

Query Match	34.1%	Score 395.4;	DB 8;	Length 413;
Best Local Similarity	97.3%;	Pred. No. 5.3e-79;		
Matches 402;	Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0

QY	3	AAACATCTACGTCAAAAATCCGAGCTCACAATCTCAATTTATGCAACTCAATCAGTAA	62
Db	413	CAACATCTACGTCAAAAATCCGAGCTCACAATCTCAATTTATGCAACTCAATCAGTAA	354
QY	63	CATCAAAAACAGTCAAAAGTAACAAAATCAAGTCAGATTGAGCACAACAAGCCAGTAA	122
Db	353	CATCAAAAACAGTCAAAAGTAACAAAATCAAGTCAGATTGAGCACAACAAGCCAGTAA	294
QY	123	TAGAAAAATTTAACGAAAGCTCATGCTAAGCTGCGAAAAATCTTCTTAATCAAAACAGT	182
Db	293	TAGAAAAATTTAACGAAAGCTCATGCTAAGCTGCGAAAAATCTTCTTAATCAAAACAGT	234
QY	183	ACAAGAGTAATTTAGCAAAATCCGAGCAGAAAACTCTACCCAGCTCCGAAATTCACGTC	242
Db	233	ACAAGAGTAATTTAGCAAAATCCGAGCAGAAAACTCTACCCAGCTCCGAAATTCACGTC	174
QY	243	TTCACTAAAAATTTTGGAAAGGATGATCAATCCAACCCATTACACAAAATACATAATC	302
Db	173	TTCACTAAAAATTTTGGAAAGGATGATCAATCCAACCCATTACACAAAATACATAATC	114
QY	303	AAATATGCGAGATCTGTAACCTGGAAACTTTGCTTCAAGTCGAGAGAGCAAAAGGAG	362
Db	113	AAATATGCGAGATCTGTAACCTGGAAACTTTGCTTCAAGTCGAGAGAGCAAAAGGAG	54
QY	363	ATCGGAGGAAGGGGCTTAGGGTTAAGCTCAGACTTATGGAGTAAATG	415
Db	53	GATTCGGAGGAAGGGGCTTAGGGTTAAGCTCAGACTTATGGAGGATTAATG	1

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RESULT 2
BZ289690
LOCUS
DEFINITION      BZ289690          400 bp            DNA             linear    GSS 24-OCT-2007
ACCESSION
VERSION
KEYWORDS
SOURCE           Arabidopsis thaliana (chale cress)
ORGANISM         Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE        1 (bases 1 to 400)
AUTHORS          Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.-J., Parker,H., Prednis,L.,
Shim,D.P., Zimmerman,J., and Ecker,J.R.
TITLE            A Sequence-Indexed Library of Insertion Mutations in the
                Arabidopsis Genome
JOURNAL          Unpublished (2001)
COMMENT          Contact: Joseph R. Ecker
                Salk Institute Genomic Analysis Laboratory (SIGAL)
                The Salk Institute for Biological Studies
                10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                Tel.: 858 453 4100 x1752
                Fax: 858 558 6379
                Email: eckerd@salk.edu
                This is single pass sequence recovered from the left border of
                TDNA.
Class: TDNA tagged.
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FEATURES	Location/Qualifiers
source	1. .400

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1..400
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_023089.34.95.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/name="PCR was performed on Arabidopsis thaliana lines"

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each of which contains one or more TADN insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

Query Match	28.8%	Score 333.4	DB 8	Length 400
Best Local Similarity	94.1%	Pred. No. 6e-65		
Matches 368	Conservative	0	Mismatches 21	Indels 2
			Gaps	2

QY	599	CGAACAAGTCGCGACATATTCATGGATCAAAACGGCTAGTGGCGGGCTCGCTC	658
Db	1	CGAGACAAGTCGCGACATATTCATGGATCAAAACACTTATTTGGCGGGCTCTCGCTC	60
QY	659	ATGTGTCACTTGTTCCTCGTTTTTTTTTAATTTTCATAGATTCCTTTGTATTCCT	718
Db	61	ATGTGTCACTTGTTCCTCGTTTTTTTTTAATTTTCATAGATTCCTTTGTATTCCT	120
QY	719	CAATACAAATTTTTGGGCTGTATCTTGCAAACTCTTCGATTCATTCGCCAATATATAGTGA	778
Db	121	CAATACAAATTTTTGGGCTGTATCTTGCAAACTCTTCGATTCATTCGCCAATATATAGTGA	180
QY	779	CACGTGTGATCTAATTTGGTGTGTTAATGTGTAATTTAGATTCATCTCGGTTTAA	838
Db	181	CACGTGTGATCTAATTTGGTGTGTTAATTTGTAATTTAAATTTCTATTTCTCGGTTTAA	240
QY	839	AGTAATTTATATGTATCATGTTTAAACATTTGTAAGTATGATTAATTAATGATAAAT	898
Db	241	AGGAATTTATATGTATCATGTTTAAACATTTGTAAGTATGATTAATTAATGATAAAT	300
QY	899	TTAGTTGATGATTAACGTGAAGCAAAAAATGAGTATGATTAATTTGTGCTATTT	958
Db	301	TTAGTTGATGATTAACG-GAAACCAAAAATGAAATTAATTCATGATTTTGGCCTATTT	359
QY	959	TGACATATGC-GGAGATGAGCTCGGGCAT	988
Db	360	TGACATATGCGGGAAGGAGACTTCGGGCAT	390

RESULT 3				
BZ084475				
LOCUS				
DEFINITION	BZ084475	692 bp	DNA	linear
	11b6id08.g1 B.oleracea002 Brassica oleracea genomic,			GSS 10-OCT-2002
	sequence.			
ACCESSION	BZ084475			
VERSION	BZ084475.1	GI:23714246		
KEYWORDS	GSS.			
SOURCE	Brassica oleracea			
ORGANISM	Brassica oleracea			
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			
REFERENCE	1 (bases 1 to 692)			
AUTHORS	Deleahunty,K., Fewell,J.G., Fulton,L., McCombie,W.R., Miner,T.,			
	Nash,W., Rabinowicz,P.D. and Wilson,R.K.			
TITLE	Whole genome shotgun reads from Brassica Oleracea			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Richard K. Wilson			

FEATURES

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/organism="Brassica oleracea"  
/mol_type="genomic DNA"  
/db_xref="taxon:3712"  
/clone_lib="B.oleracea002"
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[illegible][illegible]

Db 1020 ADATTANMAATRTAAATWTTTKTTTKTTTKTTTKTAKTKAKAGRAMWWW 1073

RESULT 10
CNS0073W/c
LOCUS
DEFINITION
CNS0073W 922 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL066784
AL066784.1 GI:4945247
GSS.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 922)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuroyo Oosagawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1..922
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14D09"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN

Query Match 5.2%; Score 60.2; DB 9; Length 922;
Best Local Similarity 25.5%; Pred. No. 0.0055;
Matches 96; Conservative 111; Mismatches 170; Indels 0; Gaps 0;

1 CAGAAACATACCTCAAAATCCAGACTCAGCATCTCAATTAATGCAACTTCATCATGAA 60
819 MNN 760
61 AACATCAAAAACAGTCAAGTAAGTAACAAATCAAGTTCAGCAACAAAGCCAGTAAA 120
759 CCMCMCMCMCAACMCAAAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAMCC 700
121 GATAGAAAATTTAAGAACGCTCATGCTAGCTGCGCAAAATATCTCTTAATCAAAACAG 180
699 MCCMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMCCM 640
181 TAACAACGAGTAATTAAGCAAAATCCAGAGAAAATCTCAACCCAGCTCCGAATTTCAAG 240
639 AAAAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAA 580
241 TCTTCACTAAATTTTTCGAAAGAAATCGATCAATACCAACCATTTACAAATATCATGAA 300
579 MMCCASAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAA 520
301 TCAAAATGGCGAATCGTACTGGAACCTTTCTTCAAGTCGACAGAGAGAGAAAAGGA 360

Db 519 AAGCACAGGCGGAGRGCGGGG 460

QY 361 AGATCGTGGAGAAAGG 377
459 GGARRRAGAGRAGRGR 443

RESULT 11
CNS060XV/c
LOCUS
DEFINITION
CNS060XV 759 bp DNA linear GSS 05-JUL-2001
T7 end of clone AM0A009H09 of library AM0A from strain CLB 89 of
Yarrowia lipolytica, genomic survey sequence.
AL411257
AL411257.1 GI:12180512
GSS.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Yarrowia lipolytica
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
1 (bases 1 to 759)
Soucier,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Boletín-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durren,P., Lepingle,A., Llorante,B.,
Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Takata,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts : 1. A set of
yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)
20584711
MEDLINE
11152876
2 (bases 1 to 759)
Casaregola,S., Neuvéglise,C., Lepingle,A., Bon,E., Feynerol,C.,
Artiguenave,F., Wincker,P. and Galliardin,C.
Genomic exploration of the hemiascomycetous yeasts : 17. Yarrowia
lipolytica
FEMS Lett. 487 (1), 95-100 (2000)
20584727
PUBMED
11152892
3 (bases 1 to 759)
Genoscope.
Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
Location/Qualifiers
1..759
/organism="Yarrowia lipolytica"
/mol_type="genomic DNA"
/strain="CLB 89"
/db_xref="taxon:4952"
/clone="AM0A009H09"
/clone_lib="AM0AA"
/note="end : T7"

ORIGIN

Query Match 5.2%; Score 60; DB 9; Length 759;
Best Local Similarity 41.0%; Pred. No. 0.006;
Matches 123; Conservative 36; Mismatches 141; Indels 0; Gaps 0;

660 TGTGACCTTGTTCCTCGTTTCTTTTAAATTTTCAATGAAGTCTTTTGTATCTTC 719
| | | | | : | | | | | | | | | | | | | | | | | | | | | : |

Query Match	Score	DB	Length
Best Local Similarity	46.28	Pred No. 0.0077	
Matches 108	Conservative 14	Mismatches 112	Indels 0
		Gaps 0	

Db	Query	Score	DB	Length
660	TGTCACCTTGGTCTCGTTTCTTTTAAATTTTCATTAAGTCTTTGTTTATCTTC	719		
263	TTCTTAATT	204		
720	AATACAAATTTTGGCGTGTATCTTGCAACTCTTCATCATATCGCAATATAGTGAAC	779		
203	TTTTTAATTTTTTGGTTTTTTTTTTTATATATTTTTTTTTTTTNCNNNTN	144		
780	ACTGATCATCAATTTGTGTGTTAAATTTAGATTCATCTCGGTTTAA	839		
143	NTTGGTGGGTATATATTTATTTGTTTACTGNTTTTTTTTTTTTTTTTTTTT	84		
840	GTGAATTAATGATCATGTGTTAAACATTTGTAAGTATGATATATGA	893		
83	TTGATTTTTTTTTTTTAAAGTGAATTKWTAAAMAAANDBKADNNNNND	30		

Db	Query	Score	DB	Length
CL648142	1187 bp DNA linear GSS 06-JUL-2004			
LOCUS	CH213-164G18 3', genomic survey sequence.			
DEFINITION	CH213-164G18 3', genomic survey sequence.			
ACCESSION	CL648142			
VERSION	CL648142.1 GI:49667566			
KEYWORDS	GSS.			
SOURCE	Gasterosteus aculeatus (three spined stickleback)			
ORGANISM	Gasterosteus aculeatus			
REFERENCE	Gasterosteus aculeatus			
AUTHORS	Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;			
TITLE	Actinopterygii; Neopterygii; Teleostei, Euteleostei, Neoteleostei;			
JOURNAL	Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;			
COMMENT	Gasterosteidae; Gasterosteus.			
	1 (bases 1 to 1187)			
	Kingley, D., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.			
	Expressed sequence tags from Gasterosteus aculeatus			
	Unpublished. (2004)			
	Contact: Grimwood, Jane			
	Stanford Human Genome Center			
	Stanford University School of Medicine			
	975 S California Avenue, Palo Alto, CA 94304, USA			
	Tel: 650 320 5917			
	Fax: 650 320 5801			
	Email: jane@shgc.stanford.edu			
	Plate: 164			
	Class: BAC ends			
	High quality sequence start: 12			
	High quality sequence stop: 664.			
	Location/Qualifiers			
	1..1187			
	/organism="Gasterosteus aculeatus"			
	/mol_type="genomic DNA"			
	/strain="Salmon River"			
	/db_xref="taxon:69293"			
	/clone="CH213-164G18"			
	/sex="Mixed"			
	/cell_type="Blood"			
	/clone_11b="CH213"			
	/note="Vector: pTRAPAC.1, Site_1: EcoRI. The sequence of			
	the clone was established as a mapping and sequencing			
	collaboration at the Stanford Genome Evolution Center,			
	funded by the NIH Centers of Excellence in Genomic Science			
	(CEGS) initiative (http://cegs.stanford.edu). The clone			
	was isolated from the BAC library CHORI-213 built by			
	Peter deLong in collaboration with the Stanford Genome			
	Evolution Center (http://www.chori.org/bacpac/). Clones			
	may be purchased from BACPAC Resources			
	(http://www.chori.org/bacpac/ordering_information.htm)."			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Db	Query	Score	DB	Length
5.18	Score 59.4	DB 9	Length 1187	
51.48	Pred. No. 0.0086			

Query Match	Score	DB	Length
Best Local Similarity	46.28	Pred No. 0.0077	
Matches	108	Conservative	14; Mismatches 112; Indels 0; Gaps 0

Db	Accession	Definition	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
660	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
263	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
720	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
203	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
780	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
143	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
840	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
83	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					

Db	Accession	Definition	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
660	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
263	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
720	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
203	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
780	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
143	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
840	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
83	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					

Db	Accession	Definition	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
660	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
263	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
720	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
203	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
780	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
143	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
840	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
83	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					

Db	Accession	Definition	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
660	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
263	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
720	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
203	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
780	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
143	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
840	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
83	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					

Db	Accession	Definition	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
660	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
263	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
720	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
203	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					
780	U00001.1	Genome of Escherichia coli O157:H7	1		GenBank	Escherichia coli					

Matches 132; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 657 TCATGTGACCTGTTTCCTGTTTTTTTAAATTTTCATTAAGTCTTTGTTTATC 716
Db 896 TAAATTTTAAATGATTTATTTATTTATTTTATTTTGAATTTATTTATTTATTT 955
QY 717 TTCAATACAAATTTTGGCTGATCTTGCAAACTTTGATCAATGCCAATATAGTG 776
Db 956 TTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1015
QY 777 AACACGTGATCAATTTGTTGTTATTTGTTAAATTTGATTCATTCGCGTTTA 836
Db 1016 AACTTTAAGATTTATTTTGGTATTTTATTTTATTTATTTATTTATTTATTTT 1075
QY 837 AAAGTGAATTAATGATCATGTTTAAACATTTGTAAGTAAAGTAAATTAATGATTA 896
Db 1076 TAAAGATTTATTTAATTAATGATTTATTTATTTTAAATATAGTTTATTAATATAT 1135
QY 897 ATTTAGTTGATGATTA 913
Db 1136 TTNTAINTATTATTTAA 1152

RESULT 14
CNS020K7/c 1092 bp DNA linear GSS 01-SEP-2000
LOCUS
DEFINITION Tetradon nigriviridis genome survey sequence T7 end of clone
22211 of library G from Tetradon nigriviridis, genomic survey
sequence.

ACCESSION AL175696.1 GI:7813753
VERSION
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigriviridis
ORGANISM Tetradon nigriviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE 1
Roest Crolius,H., Jallou,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Broctier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigriviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL MEDLINE 20296633
PUBMED 10835645

REFERENCE 2
Roest Crolius,H., Jallou,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigriviridis
Genome Res. 10 (7), 939-949 (2000)

JOURNAL MEDLINE 20359837
PUBMED 10899143

REFERENCE 3 (bases 1 to 1092)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigriviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
Location/Qualifiers
1..1092
/organism="Tetradon nigriviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="22211"
/clone_lib="G"

FEATURES
source

ORIGIN /note="Genoscope sequence ID : C0AG222CF06LP1-end : T7"

Query Match 5.1%; Score 59.2; DB 9; Length 1092;
Best Local Similarity 39.9%; Pred. No. 0.0095;
Matches 123; Conservative 47; Mismatches 137; Indels 1; Gaps 1;

QY 659 ATGTGTACCTGTTTCCTGTTTTTTTAAATTTTCATTAAGTCTTTGTTTATCTT 718
Db 1025 ATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 966
QY 719 CAATACAAATTTTGGCTGATCTTGCAAACTTCGATCATCGCAATATGCGTAA 778
Db 965 TTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 907
QY 779 CACTGTCATCAATTTGTTGTTTAAATTTGTTAAATTTAGATTCATTCGCGTTTAA 838
Db 906 AAAAAAAMWTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAAW 847
QY 839 AGTGAATTATATGATCATGTTTAAACATTTGTAAGTAAATGATTAATGATTAAT 898
Db 846 AATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 787
QY 899 TTAGTGAATGATTAACGGAAGCAAAATGAGTAAATGATTTGATTTGCTATTT 958
Db 786 WTAAMAMWTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 727
QY 959 TGACATAT 966
Db 726 TAAATTTT 719

RESULT 15
CNS03YB4/c 1045 bp DNA linear GSS 01-SEP-2000
LOCUS
DEFINITION Tetradon nigriviridis genome survey sequence T7 end of clone
068003 of library G from Tetradon nigriviridis, genomic survey
sequence.

ACCESSION AL266197.1 GI:7987962
VERSION
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigriviridis
ORGANISM Tetradon nigriviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE 1
Roest Crolius,H., Jallou,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Broctier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetradon nigriviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL MEDLINE 20296633
PUBMED 10835645

REFERENCE 2
Roest Crolius,H., Jallou,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigriviridis
Genome Res. 10 (7), 939-949 (2000)

JOURNAL MEDLINE 20359837
PUBMED 10899143

REFERENCE 3 (bases 1 to 1045)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigriviridis

COMMENT

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 02:07:01 ; Search time 728 Seconds
(without alignments)
9416.292 Million cell updates/sec

Title: US-09-998-059-1

Perfect score: 1158
Sequence: 1 cacaacacatcacctcaaat.....ctctcacaacaacaagaag 1158

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_16dec04:*
2: geneeqn1980s:*
3: geneeqn1980s:*
4: geneeqn2000s:*
5: geneeqn2000s:*
6: geneeqn2000s:*
7: geneeqn2000s:*
8: geneeqn2000s:*
9: geneeqn2000s:*
10: geneeqn2000s:*
11: geneeqn2000s:*
12: geneeqn2000s:*
13: geneeqn2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1158	100.0	1164	10	ADJ19001
2	1158	100.0	1223	6	ABZ17132 Arabidops
3	1064	91.9	1067	13	ADR89446
4	81	7.0	1118	3	AAC33222 Arabidops
5	65.4	5.6	10326	6	ABL34166 Human imm
6	64.2	5.5	547	13	ACN62109
7	56.4	4.9	433	13	ACN51900
8	56.2	4.9	6000	6	ABL33133
9	55.8	4.9	40324	6	ABO67149 Human ang
10	55.8	4.8	5845	6	ABL33662 Human imm
11	54.6	4.7	3476	13	ADN89736
12	54.6	4.7	7441	6	ABK40058 Human che
13	54.6	4.7	7479	6	AA653345 Chemical
14	54.2	4.7	6713	6	ABL33080 Human imm
15	54.2	4.7	6713	6	ABL34526 Human met
16	54.2	4.7	6713	6	ABL70251 Chemical
17	54.2	4.7	6713	7	ADN99787 Bismulphit
18	53.6	4.6	7215	6	ABN91164 Staphyloc
19	53.6	4.6	7215	13	ADN501346
20	53.4	4.6	520	13	ACN52918 Cotton an

C	21	53.4	4.6	29993	10	ADB37662	Ad337662 Human che
	22	52.4	4.5	2000	8	ADA71938	Ad71938 Rice gene
	23	52.2	4.5	337	8	ABX41811	Abx41811 Bovine ES
	24	52	4.5	694	4	AAH53104	Aah53104 S. epider
	25	52	4.5	875	4	AAI95044	Aai95044 Human neu
	26	52	4.5	3028	4	AAH54496	Aah54496 S. epider
	27	52	4.5	3032	4	AAH54863	Aah54863 S. epider
	28	52	4.5	6968	4	AAH52683	Aah52683 S. epider
C	29	51.2	4.4	529	13	ACN56029	Acn56029 Cotton an
	30	51.2	4.4	96588	9	ADA03026	Ada03026 Human MBN
	31	51.2	4.4	96588	10	ADB72764	Ad72764 Human MBN
	32	51.2	4.4	96588	10	ADC85506	Adc85506 Human MBN
	33	51.2	4.4	96588	12	ADM74621	Adm74621 Human car
C	34	51	4.4	11735	6	AAH53328	Aah53328 Chemical
C	35	51	4.4	11735	6	ABK28167	Abk28167 DNA trans
C	36	51	4.4	11735	6	AAH56141	Aah56141 Human gen
C	37	51	4.4	13511	6	ABL32280	AbL32280 Human imm
C	38	50.8	4.4	6621	8	ABZ10129	Abz10129 Haematopo
C	39	50.8	4.4	6621	8	ABZ10243	Abz10243 Haematopo
C	40	50.8	4.4	6621	10	ADE84153	Ad84153 Human lym
C	41	50.6	4.4	3683	8	ABZ10199	Abz10199 Haematopo
C	42	50.6	4.4	8011	6	ABL32078	AbL32078 Human imm
	43	50.6	4.4	8011	6	AAZ28368	Aaz28368 Human che
	44	50.4	4.4	419	8	ABX46069	Abx46069 Bovine ES
	45	50.4	4.4	7544	4	AAH545300	Aah545300 Chemical

ALIGNMENTS

RESULT 1	ADJ19001	ADJ19001 standard; DNA; 1164 BP.
ID	ADJ19001	
XX	ADJ19001	
AC	ADJ19001	
XX	ADJ19001	
DT	20-MAY-2004	(first entry)
XX		
DE	Thale cress seed-specific promoter region Pl DNA.	
XX		
KM	plant; seed-specific promoter region; seed development; food;	
KW	agricultural; thale cress; ds; Pl.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	US2003005485-A1.	
XX		
PD	02-JAN-2003.	
XX		
PF	30-NOV-2001; 2001US-00998059.	
XX		
PR	01-DEC-2000; 2000US-0250401P.	
XX		
PA	(OHLE/) OHLEGE J B.	
XX		
PA	(BENN/) BENNING C.	
XX		
PA	(GAOH/) GAO H.	
XX		
PA	(GIRK/) GIRKE T A A.	
XX		
PA	(WHIT/) WHITE J A.	
XX		
PI	Chloogy JB, Benning C, Gao H, Girke TAA, White JA;	
XX		
DR	WPI; 2003-370848/35.	
XX		
PT	New DNA comprising plant seed specific promoters, useful for controlling	
XX		
PT	expression of genes in plants, particularly for modifying seed products	
XX		
PT	(proteins, carbohydrates or oils), which are of major economic and food	
XX		
PS	values.	
XX		
PS	Claim 1: SEQ ID NO 1; 57bp; English.	
XX		
CC	The invention relates to a novel isolated DNA molecule which comprises a	
XX		
CC	plant seed-specific promoter region. The DNA molecule of the invention	
XX		
CC	may be useful for controlling the expression of genes in plants during	
XX		
CC		

the different phases of seed development, in particular, for modifying seed products, which are the major economic and food values of most agricultural plants e.g. as sources of proteins, carbohydrates or oils. The current sequence is that of the thale cress seed-specific promoter region P1 DNA of the invention.

Sequence 1164 BP, 399 A; 228 C; 205 G; 332 T; 0 U; 0 Other;

Query Match 100.0%; Score 1158; DB 10; Length 1164;
Best Local Similarity 100.0%; Pred. No. 5.2e-250;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CACAAACATACATCAAAATCCAGCTCACTCACTCAATTAATGCAATTCATCATGAA 60
DB 1 CACAAACATACATCAAAATCCAGCTCACTCACTCAATTAATGCAATTCATCATGAA 60
QY AACATCAAAAACAGTCAAAAGTAACAAATCAAGTCAAGTCAAGCAAGCAAGCCGATGAA 120
DB AACATCAAAAACAGTCAAAAGTAACAAATCAAGTCAAGTCAAGCAAGCAAGCCGATGAA 120
QY 121 GATAGAAAATTTAAAGAAAGCTCATGCTAGCTGCGCAAAATTAATCTTAATCAAAACAG 180
DB 121 GATAGAAAATTTAAAGAAAGCTCATGCTAGCTGCGCAAAATTAATCTTAATCAAAACAG 180
QY 181 TAAACAAGAGTAATTAAGCAAAATCCAGCAAGAAATCTCAACCCACCTCCGAATTCACG 240
DB 181 TAAACAAGAGTAATTAAGCAAAATCCAGCAAGAAATCTCAACCCACCTCCGAATTCACG 240
QY 241 TCTTCACTAAATTTGCAAAAGGAATGATCAATCCCAATTAATCAAAATTCATGAA 300
DB 241 TCTTCACTAAATTTGCAAAAGGAATGATCAATCCCAATTAATCAAAATTCATGAA 300
QY 301 TCAAAATGCGAGAAATCGTACCTGGAACCTTTCCTCAAGTCGAGAGAGAGAAAGGA 360
DB 301 TCAAAATGCGAGAAATCGTACCTGGAACCTTTCCTCAAGTCGAGAGAGAGAAAGGA 360
QY 361 AGATCGTGAAGAAAGGGTTTAAAGGTTAAAGTCAAGTCTTATTTAGTAATGGACG 420
DB 361 AGATCGTGAAGAAAGGGTTTAAAGGTTAAAGTCAAGTCTTATTTAGTAATGGACG 420
QY 421 GTGTCACTTTTCGTTTGGAAATGAACCTTGGGCTACAGTTAGGGCTATTAGATTT 480
DB 421 GTGTCACTTTTCGTTTGGAAATGAACCTTGGGCTACAGTTAGGGCTATTAGATTT 480
QY 481 TGATGGGCTTTCTAGTAATTAACAATATAAGTTATGGCTTAAGTTAATAGCCCATGT 540
DB 481 TGATGGGCTTTCTAGTAATTAACAATATAAGTTATGGCTTAAGTTAATAGCCCATGT 540
QY 541 TGAATAATTTTGAACATGCTTGGCTACTAGTCTAAACATGCAACCGAACAGTTGTG 600
DB 541 TGAATAATTTTGAACATGCTTGGCTACTAGTCTAAACATGCAACCGAACAGTTGTG 600
QY 601 AGACAAGTCGAGCAATATCAATGATGCAACAGCCGTAAGTCCGCGCTGCTCAT 660
DB 601 AGACAAGTCGAGCAATATCAATGATGCAACAGCCGTAAGTCCGCGCTGCTCAT 660
QY 661 GTGTCACTTTTCGTTTGGAAATGAACCTTGGGCTACAGTTAGGGCTATTAGATTT 720
DB 661 GTGTCACTTTTCGTTTGGAAATGAACCTTGGGCTACAGTTAGGGCTATTAGATTT 720
QY 721 ATACAAATTTTGGCTGTATCTTGAACACTCTTGATCATATCGCAATATACGTAACA 780
DB 721 ATACAAATTTTGGCTGTATCTTGAACACTCTTGATCATATCGCAATATACGTAACA 780
QY 781 CTGGGATCTAATTTGTGTGTAATGTAATTAATTAATTAATTAATTAATTAATTAAG 840
DB 781 CTGGGATCTAATTTGTGTGTAATGTAATTAATTAATTAATTAATTAATTAATTAAG 840
QY 841 TGAATTAATATATATATATATATATATATATATATATATATATATATATATATAT 900
DB 841 TGAATTAATATATATATATATATATATATATATATATATATATATATATATATAT 900
QY 901 AGTTGATGATTAACGTGAAGCAAAATGAGATGATGATGATGATGATGATGATGAT 960

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DB 901 AGTTGATGATTAACGTGAAGCAAAATGAGATGATGATGATGATGATGATGATGAT 960
QY 961 ACATATGCGAGAGTGAAGCTACGCGCATGGAAGATCAAGACACATGCTGAGCTCAAG 1020
DB 961 ACATATGCGAGAGTGAAGCTACGCGCATGGAAGATCAAGACACATGCTGAGCTCAAG 1020
QY 1021 AGTACGTGTAAAAAGCTTAACTGAAGTCCCATGCAAACTTAATCTTACGTGGCTGAA 1080
DB 1021 AGTACGTGTAAAAAGCTTAACTGAAGTCCCATGCAAACTTAATCTTACGTGGCTGAA 1080
QY 1081 ACCACGAGCTCACTTGAACAATATTAATCTCTTAACTGCTGCTTCTTCAATCATCT 1140
DB 1081 ACCACGAGCTCACTTGAACAATATTAATCTCTTAACTGCTGCTTCTTCAATCATCT 1140
QY 1141 CTCACAAACAAACAAAG 1158
DB 1141 CTCACAAACAAACAAAG 1158

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RESULT 2
AB217132
ID AB217132 standard; DNA; 1223 BP.
XX
AC AB217132;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4937.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN MO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCRI ) SCRIPPS RES INST.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
PI Harper JF, Krepe J, Wang X, Zhu T;
XX
XX WPI; 2002-304127/34.
DR
PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
XX Claim 144; SEQ ID NO 4937; 577bp + Sequence Listing; English.
XX
XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising: (a) contacting nucleic acid
XX representative of expressed polynucleotides in the plant cell with an
XX array or probes representative of the plant cell genome; and (b)
XX detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
XX in methods of the invention. Note: the sequence data for this patent is
XX not represented in the printed specification but is based on sequence
XX information supplied to Derwent by the European Patent Office

```

Query Match 100.0%; Score 1158; DB 6; Length 1223;
Best Local Similarity 100.0%; Pred. No. 5.2e-250;

QY 155 CGCAAAATACCTTCTTAATCAAAACGTAACAACGTAATTAGCAAAATCCGAGCAGAAA 214
Db 61 CGCAAAATACCTTCTTAATCAAAACGTAACAACGTAATTAGCAAAATCCGAGCAGAAA 120
QY 215 ACTGCACCCACCTCCGAAATTCACGCTCTCACTAAATTTTTCGAAAGAAATCCGATCAT 274
Db 121 ACTGCACCCACCTCCGAAATTCACGCTCTCACTAAATTTTTCGAAAGAAATCCGATCAT 180
QY 275 ACCAACCATTACACAAATATCATATCAAAATGCGAAGATCGTACCTGGAACTTTGC 334
Db 181 ACCAACCATTACACAAATATCATATCAAAATGCGAAGATCGTACCTGGAACTTTGC 240
QY 335 TTCAGTGGCAGAGAGAGAGAGAGAGAGATGTGAGAGAAAGGGGTTTGCGTTTAAGCTC 394
Db 241 TTCAGTGGCAGAGAGAGAGAGAGAGATGTGAGAGAAAGGGGTTTGCGTTTAAGCTC 300
QY 395 AGACTTCTATTGGAGTAATGGGACGCTGTCACATTTCCGTTTGGAAATGAATCTTGG 454
Db 301 AGACTTCTATTGGAGTAATGGGACGCTGTCACATTTCCGTTTGGAAATGAATCTTGG 360
QY 455 GCTCAGCTTATGGGCTATTAGATATTTGATGGGCTTTCTAGTAATAATCAATATAATTAT 514
Db 361 GCTCAGCTTATGGGCTATTAGATATTTGATGGGCTTTCTAGTAATAATCAATATAATTAT 420
QY 515 TGGGCTTATGTTAAATAAGCCCATGTTGAAATATTTGACACATGCTTGGCTACTAGTG 574
Db 421 TGGGCTTATGTTAAATAAGCCCATGTTGAAATATTTGACACATGCTTGGCTACTAGTG 480
QY 575 CTAAACATGCAACCGAAGTGTGAGACAAAGTGGAGCAATATTCATATGATGATCAACAC 634
Db 481 CTAAACATGCAACCGAAGTGTGAGACAAAGTGGAGCAATATTCATATGATGATCAACAC 540
QY 635 GCCATAGTGCAGCGCTGCTCATGTGTCACCTTGTTCCTCGTTTCTTTTAAATTT 694
Db 541 GCCATAGTGCAGCGCTGCTCATGTGTCACCTTGTTCCTCGTTTCTTTTAAATTT 600
QY 695 TCATTAAGTCTTTTGTATTTTCTTAATCAATCAAAATTTTGGCTGTAATCTGCAACTTTC 754
Db 601 TCATTAAGTCTTTTGTATTTTCTTAATCAATCAAAATTTTGGCTGTAATCTGCAACTTTC 660
QY 755 GATCATATGCGCAATATAGTGAACACTGAGTATATTTGTTGTTATTTGTTAAT 814
Db 661 GATCATATGCGCAATATAGTGAACACTGAGTATATTTGTTGTTAATTTGTTAAT 720
QY 815 TTAGATTTCTATTCCTCGGTTTAAAGTGAATTAATATGATGATGTTTAAACATTTGTAAG 874
Db 721 TTAGATTTCTATTCCTCGGTTTAAAGTGAATTAATATGATGATGTTTAAACATTTGTAAG 780
QY 875 TAAAGTGAATTAATAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 934
Db 781 TAAAGTGAATTAATAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
QY 935 GATACATTTGATTTTGTGCTATTTTGAATATGCGAGAGTGAAGTACGCGCATGAAGAT 994
Db 841 GATACATTTGATTTTGTGCTATTTTGAATATGCGAGAGTGAAGTACGCGCATGAAGAT 900
QY 995 CAAGAGCACTTGTGCTGAGCTCAGAGTGAAGTGAATTAATTAATTAATTAATTAATTAAT 1054
Db 901 CAAGAGCACTTGTGCTGAGCTCAGAGTGAAGTGAATTAATTAATTAATTAATTAATTAAT 960
QY 1055 TGCAAACTTAATCTCAAGTGTCAAAACGAGAGTCACTTGACATATTAATTAATTAATTAAT 1114
Db 961 TGCAAACTTAATCTCAAGTGTCAAAACGAGAGTCACTTGACATATTAATTAATTAATTAAT 1020
QY 1115 CTAGTCCCGTCTCTTCAATCTCAATCTCAAAACAAATTAATTAATTAATTAATTAATTAAT 1158
Db 1021 CTAGTCCCGTCTCTTCAATCTCAATCTCAAAACAAATTAATTAATTAATTAATTAATTAAT 1064

RESULT 4
AAC33222/C
ID AAC33222 standard; DNA; 1118 BP.
XX

AC AAC33222;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 2235.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
OS Arabidopsis thaliana.
EN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126254P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139482P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.

XX Human immune system associated gene SEQ ID NO: 2139.
DE
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianemic; cytosinergic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antirhectic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PP 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR MPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 2139; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC leukaria degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
CC
SQ Sequence 10326 BP; 2542 A; 104 C; 2689 G; 4991 T; 0 U; 0 Other;
Query Match 5.6%; Score 65.4; DB 6; Length 10326;
Best Local Similarity 48.8%; Pred. No.0.00013;
Matches 177; Conservative 0; Mismatches 186; Indels 0; Gaps 0;
QY 2 ACACACATACACTCAAAATCCAGATCACTCACTCAATTAATGCACTTCATCATGAA 61
DB 2764 ACCAAGCTAAGCTCAAAAACCCCACTAAATTAATAACCTTAACAAAATTTCAACTAT 2705
QY 62 ACATCAAAAAGCTCAAAAGTAACTCAAGTCAGATTCAGACACAAAGCCGTAAG 121
DB 2704 TCACCTCAAAAACAAAATTTTCTACTCACTAAATTAACAAAACAAAACAAAATTA 2645
QY 122 ATAGAAATTTAAGCAAGCTCAGCTAGCTGCGCAAAATTAATCTCCATATCAAAACGT 181
DB 2644 AAAAATTTTAAACACCCCTCCAAAAATTAACAAAACACAAATCTCAACAAATTA 2585
QY 182 AACACAGATTAATAGCAAAATCCGAGAGAAAATCTCACCACCTCCGAAATTCAGGT 241
DB 2584 TACCATTCACAATTTCTAAATTAATAAATTTATCAAAACATTAATAAAAAATACTA 2525
QY 242 CTTCACTAAATTTTTCGAAGATCGATCAATACCAACCATTAACAAAATATCATAT 301
DB 2524 TATCAACCATTAATTAATAAATAATATCAATAAATAATTAATTAATTAATTAAT 2465
QY 302 CAAATATGCGGAGATTCGATCTCGGAACTTTGCTTCAAGTCGACAGAGAGAGAAAAGAA 361
DB 2464 TAAATAATTAACAAAATTTTAAACAAATATCTTACTACTCAATATTAATAAAAAA 2405

QY 362 GAT 364
DB 2404 TAT 2402
RESULT 6
ID ACN62109 standard; cDNA; 547 BP.
ACN62109;
AC
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-N6-C2, SEQ:16890.
XX
KW Cotton; plant; EST; expressed sequence tag; transgenic plant; gynoecium;
KW variety Nucleon33B; library LIB3829; molecular tag; molecular marker;
KW genetic mapping; molecular mapping; seed germination; plant growth;
KW plant quality; plant yield; plant breeding; tissue printing; ss.
OS
XX
XX Gossypium hirsutum.
XX
PN US2004123340-A1.
XX
PD 24-JUN-2004.
XX
PF 12-DEC-2001; 2001US-00021323.
XX
PR 14-DEC-2000; 2000US-0255619P.
XX
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
XX
PI Deikman J, Peng PCC, Fincher KL, Ziegler TE;
XX
DR MPI; 2004-479808/45.
XX
CC New isolated nucleic acid molecule that encodes a plant protein or its
PT fragment, useful for isolating a variety of agronomically significant
PT genes associated with plant growth, quality or yield, and as molecular
PT tags to map genes.
XX
PS Claim 1; SEQ ID NO 16890; 34pp; English.
XX
CC The invention relates to 17880 cotton expressed sequence tags (ESTs;
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC from primed or non-primed seeds from variety DP50B, mature seeds from
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucleon33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
CC invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC molecular tags to isolate genetic regions, to isolate genes, to map
CC genes, to determine gene function and to determine whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
CC also useful for identifying genes important in initiating and maintaining
CC seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTs additionally enable the acquisition of
CC promoters and cis-regulatory elements which will be useful to express
CC agronomically significant genes in these tissues and/or other tissues,
CC and also permits the acquisition of molecular markers useful in breeding
CC schemes, genetic and molecular mapping, and in cloning of agronomically
CC significant genes. The nucleic acid molecules are further useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC present sequence represents a specifically claimed EST isolated from a

CLAIM 1; SEQ ID NO 6681; 34bp; ENGLISH
XX

KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW antineumatic; antiautumn; antidiabetic; antipsoriatic;
KW antineumatic; antiautumn; antidiabetic; antipsoriatic;
KW antineumatic; antiautumn; antidiabetic; antipsoriatic;

KW		acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KM		neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
XX		ds.
OS	Homo sapiens.	
PX		
PN	WO20020928-A2.	
XX		
PD	03-JAN-2002.	
XX		
PP	02-JUL-2001; 2001WO-EP007537.	
PR	30-JUN-2000; 2000DE-01032529.	
PR	01-SEP-2000; 2000DE-01043826.	
PA	(EPIG-) EPIGENOMICS AG.	
PI	Olek A, Piepenbrock C, Berlin K;	
XX		
DR	WPI; 2002-130909/17.	
PT	Nucleic acid comprising fragment of chemically modified gene, useful for	
PT	diagnosis and treatment of diseases associated with abnormal cytosine	
XX	methylation.	
XX		
PS	Claim 1; SEQ ID NO 1106; 32pp + Sequence Listing; German.	
CC	The present invention provides a number of human immune system associated	
CC	genes which are modified by the methylation of cytosines. The sequences	
CC	can be used in the diagnosis and treatment of immune system disorders,	
CC	including eye diseases such as retinopathy, neovascular glaucoma and	
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid	
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,	
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel	
CC	diseases. The present sequence is a gene of the invention	
SQ	Sequence 6000 BP; 1186 A; 274 C; 1753 G; 2787 T; 0 U; 0 Other;	
Query Match	4.9%; Score 56.2; DB 6; Length 6000;	
Best Local Similarity	51.0%; Pred. No. 0.013;	
Matches 133; Conservative	0; Mismatches 128; Indels 0; Gaps 0;	
Db		
40	ATTATGCACTTCATCATGAAAAACTCAAAAACAGTCAAAGTAACAATAATCAATCAGT	99
4828	ATTAAAAAACCNAACCGTAAACCCCTTAAACGATTCGAACGTATTTAAAAAACACTCAAC	4765
0Y	TCAGCACACAAGCCAGTAAAGATAGAATAATTTTACGAAGCTCATGCTAAGTGCGCA	159
Dd	TCAACTTACAAACCTTACAAAAAAACCTCTTAATAATTTCTCAACTTCAACTCCCTCA	47099
0Y	160 AATATCTTCTATCAAAAACAGTAAACAAGATATTAGCAAAATCCGACAGAAAACTCT	219
Dd	ATACTCACTTAATTAATTCACAAACCATATATAAAAACAAACGGCTAATCTAATCA	4649
0Y	220 CACCACCTCCGAATTTCACGCTTTCATTAATTTTGGAAAGGAATGCATCATCCCA	279
Dd	4648 TAAAAACAACAAAAACCGTATCATTTCTTAAAAATTAACAAACCTACAAAAACCA	45899
0Y	280 CCCATTACACAAAATACATAA 300	
Dd	4588 AACATCTACAAAATAATAAAA 4568	
RESULT 9		
ID	ABO67149 standard; DNA; 40324 BP.	
XX		
AC	ABO67149;	
XX		
DT	28-AUG-2002 (first entry)	
XX		
DE	Human angiogenesis associated polynucleotide SEQ ID NO 179.	
XX		

[illegible]

XX 26-MAR-2002 (first entry)
DT
XX
DE Human immune system associated gene SEQ ID NO: 1635.

XX Human; immune system disease; cytosine methylation; antiasthmatic;
XX antiarteriosclerotic; antiangioma; cytosine methylation; nootropic;
XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
XX de.

XX Homo sapiens.
OS
XX
XX WO200200928-A2.
PN
XX
XX 03-JAN-2002.
PD

XX 02-JUL-2001; 2001WO-EP007537.
PF
XX 30-JUN-2000; 2000DE-01033529.
PR
XX 01-SEP-2000; 2000DE-01043826.
PR

XX (EPIG-) EPIGENOMICS AG.
PA

XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2002-130909/17.
DR

XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

XX Claim 1; SEQ ID NO 1635; 32pp + Sequence Listing; German.
PS

XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
CC

XX Sequence 5845 BP; 1651 A; 58 C; 1168 G; 2968 T; 0 U; 0 Other;
SQ

Query Match 4.8%; Score 55.8; DB 6; Length 5845;
Best Local Similarity 49.5%; Pred. No. 0.016;
Matches 144; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 669 TTGTTTCCTCGTTTTTTTAAATTTTCATTAAGTCTTTGTTTATCTTCATACAAAT 728
DB 634 TTTTCTT 693
QY 729 TTTTGGCTATCTTGCACACTCTTCGATCATATGCCCAATATAGTGAACACTGTGAT 788
DB 634 TTTTCTT 753
QY 789 CTAAATTTGTTGTTAATTTTAAATTTAGATTCATTCGCGTTAAAGATTAAT 848
DB 754 TTTTCTT 813
QY 849 ATGTATCATGTTAAACATTTGATTAAGATTAATTAATAAATGATTAATTTAGTTGATG 908
DB 814 AATTTTCTTTAGATTAAGATTAAGATTAATTTTAAATTTTAAATTTTAAATTTTAAAT 873
QY 909 GATTAACGTAAAGCAAAATGATATGATATCAATTTTATTTGCGATTTT 959
DB 874 TGTATTTTATTAAGATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 924

RESULT 11
ADS89736
ID ADS89736 standard; DNA; 3476 BP.

XX ADS89736;
AC

XX 18-NOV-2004 (first entry)
DT

XX Oligonucleotide of the invention SEQ ID NO:752.
DE

XX ss; cell proliferative disorder; breast; methylation; cytosine;
XX gene therapy; single nucleotide polymorphism; SNP.
XX

XX Unidentified.
OS

XX WO2004035803-A2.
PN

XX 29-APR-2004.
PD

XX 01-OCT-2003; 2003WO-EP010881.
PF

XX 01-OCT-2002; 2002DE-01045779.
PR

XX 07-JAN-2003; 2003DE-01000096.
PR

XX 17-APR-2003; 2003DE-01017955.
PR

XX (EPIG-) EPIGENOMICS AG.
PA

XX Foekens J, Harbeck N, Koenig T, Maier S, Martens J, Model F;
PI
XX Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
PI

XX WPI; 2004-348468/32.
DR

XX Predicting responsiveness of a subject with breast cell proliferative
PT disorder, useful for treating or differentiating breast cell
PT proliferative disorders comprises analyzing methylation pattern of a
PT genomic DNA from the subject.
PT

XX Disclosure; SEQ ID NO 752; 104pp; English.
PS

XX The invention relates to a novel method for predicting the responsiveness
CC of a subject with a cell proliferative disorder of the breast tissues to
CC a therapy comprising analysing the methylation pattern of a target
CC nucleic acid by contacting at least one of the target nucleic acids in a
CC biological sample obtained from the subject prior to or during treatment.
CC The method of the invention has cytosine activity, and may have a use
CC in gene therapy. The set of oligonucleotides comprising at least two of
CC the oligomers are useful for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
CC methods, nucleic acid, oligonucleotide, and kit are useful for the
CC treatment, characterisation, classification and/or differentiation, of
CC breast cell proliferative disorders. The method is also useful for
CC predicting the responsiveness of a subject with a cell proliferative
CC disorder of the breast tissues to a therapy. The present sequence is used
CC in the exemplification of the invention.
CC

XX Sequence 3476 BP; 821 A; 0 C; 861 G; 1794 T; 0 U; 0 Other;
SQ

Query Match 4.7%; Score 54.6; DB 13; Length 3476;
Best Local Similarity 51.2%; Pred. No. 0.026;
Matches 152; Conservative 0; Mismatches 144; Indels 1; Gaps 1;

QY 669 TTGTTTCCTCGTTTTTTTAAATTTTCAATAGTCTTTGTTTATCTTCATACAAAT 728
DB 2114 TTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2173
QY 729 TTTTGGCTATCTTGCACACTCTTCGATCATATGCCCAATATAGTGAACACTGTGAT 788
DB 2174 AATAGATTTATTAAGAAATTTTGGTGAAGGAAATAGTGAATTTAAGAA 2233
QY 789 CTAAATTTGT-TGTGTTAATTTTAAATTTAGATTCATTCGCGTTAAAGATTA 847
DB 2234 GTTGTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2293

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QY      848 TATGATCATGCTTAAACATTGTAAGTATGATATATAATGATTAATTGATGAT 907
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2294 TTTTTCGATGATTTAAGAAATTAATGATATTTAGATTAAGATATAGAGAT 2353
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      908 GGATTAAGTGAGAGAAAAATGAGATGATCATTGATTTTGTCGATTTTGACAT 964
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2354 GGAGAAATGTTGTGATGATGAGAAAAATATGATTTTAAATTGATATGATATAT 2410
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
ABK40058
ID      ABK40058 standard; DNA; 7441 BP.
XX
AC      ABK40058;
XX
DT      21-MAY-2002 (first entry)
XX
DE      Human chemically pretreated gene sequence #70 strand 2.
XX
KW      Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
KM      cytosstatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCIN; TXNRD1;
KW      UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
XX
OS      Homo sapiens.
XX
PN      WO200202806-A2.
PD      10-JAN-2002.
PF      29-JUN-2001; 2001WO-EP007470.
PR      30-JUN-2000; 2000DE-01032529.
PR      01-SEP-2000; 2000DE-01043826.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
DR      WPI; 2002-154757/20.
XX
PT      New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers,
        useful for detecting cytosine methylation state of genes associated with
        pharmacogenomics and for therapy of diseases e.g. cancer.
XX
PS      Claim 1; SEQ ID NO 140; 24pp; English.
XX
CC      The invention relates to a nucleic acid comprising a sequence at least 18
        bases in length of a segment of the chemically pretreated DNA of genes
        associated with pharmacogenomics according to one of the sequences of the
        genes ALDH6 (NM_000693), CYP11A (NM_000781), CYP11B1 (NM_000497), CYP3A3
        (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2 (NM_001979), OCIN
        (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360), MRP (NM_004596,
        NM_019900, NM_019901, NM_019902, NM_019862, NM_019898, NM_019899) and
        their complementary sequences, or a sequence (S1) chosen from 87
        sequences and their pretreatments. The chemical pretreatment is bisulphite
        treatment to convert cytosines (but not methyl-cytosines) into uracils.
        Also included are an oligomer (II) in particular an oligonucleotide or a
        peptide nucleic acid (PNA)-oligomer, comprising in each case at least one
        base sequence having a length of 9 nucleotides which hybridises to or is
        identical to a chemically pretreated DNA of genes associated with
        pharmacogenomics and their complements, arranged in an array for
        analysing diseases associated with the methylation state (CpG) and/or
        detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The
        oligomers may also be used as PCR primers. The set of 87 nucleic acids
        and their complements is useful for diagnosis and therapy of solid
        tumours and cancer. The present sequence represents one the 87 DNA
        sequences or its complement. Note: The sequence data for this patent did
        not form part of the printed specification, but was obtained in
        electronic format directly from WIPO at
        ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 7441 BP; 2128 A; 66 C; 1267 G; 3980 T; 0 U; 0 Other;
```

```
Query Match      4.7%; Score 54.6; DB 6; Length 7441;
Best Local Similarity 48.8%; Pred. No. 0.031;
Matches 147; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY      657 TCATGTCACCTGTTTCCGCTTTTCTTTTAAATTTTCATAGTCTTTGTTTATC 716
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      6941 TTATTATTTTGTGTTTAAATTTAAATGATGTTTTTAAATTTTATATTTTGA 7000
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      717 TTCATACAAATTTTGGCTGATCTTGCAACTCTTCGATCATATGCCAATATACGTG 776
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      7001 TTTTAAATTTTGTGTTTATTTTGGAATAATTCGATATTTTAAAGTTAGT 7060
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      777 AACACTGCTGATCTAAATTTGTTGTTATTTGTTAAATTTGATTCATCTCCGTTTA 836
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      7061 TATTGGCGCTATTAATTAAGGTTTAAAGATGATGTTTATTTTGGATAGGTTT 7120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      837 AAAGTGAATTAATGATCATGTTAAACCTGTAAGTATGATGATTAATAATGATTA 896
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      7121 TGTTAGTAAATTTTGTATTTTATTTTAAATTTTTTTATTTTAAATGTTAA 7180
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      897 ATTATGTTGATGATTAACGTGACCAAAATGAGATGATACATTTGATTTGTCGTAT 956
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      7181 TTTGTTTGTGTGAGTTCGTTTAAAGGATGTTAATTAATTAATTAATTAATTTT 7240
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      957 T 957
        |||
DB      7241 T 7241

RESULT 13
AAS63345
ID      AAS63345 standard; DNA; 7479 BP.
XX
AC      AAS63345;
XX
DT      29-JAN-2002 (first entry)
XX
DE      Chemically pretreated metabolism associated gene #40.
XX
KW      Human; cytosstatic; anti-tumour; metabolism; metabolic disease; liver;
        solid tumour; cancer; cytosine methylation; epigenetic; eye; kidney;
        single nucleotide polymorphism detection; SNP; stool; urine; lung;
        cerebral-spinal fluid; intestine; brain; heart; prostate; breast; DUSP2;
        EPHX2; QDPR; SGSH; SHMT2; SLC7A2; SLC7A4; TYMS; ds.
XX
OS      Homo sapiens.
XX
PN      WO200176451-A2.
PD      18-OCT-2001.
PF      06-APR-2001; 2001WO-EP004016.
PR      06-APR-2000; 2000DE-01019058.
PR      07-APR-2000; 2000DE-01019173.
PR      30-JUN-2000; 2000DE-01032529.
PR      01-SEP-2000; 2000DE-01043826.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
DR      WPI; 2002-010834/01.
XX
PT      New nucleic acid, useful for diagnosis and therapy of metabolic disease,
        solid tumor and cancers, comprises segment of chemically modified genomic
        sequences of genes associated with metabolism.
XX
PS      Claim 1; Page 109-111; 143pp; English.
XX
CC      The invention relates to a nucleic acid (I) comprising a sequence at
        least 18 bases of a segment of the chemically pretreated DNA of genes
        associated with metabolism such as DUSP2 (NM_004418), EPHX2 (NM_001979),
```


DE Human metastasis associated gene SEQ ID NO: 79.

XX Metastasis associated gene; cytostatic; gene therapy; cancer;
KW cytosine methylation; gene; ds.
XX

OS Homo sapiens.

XX WO20017376-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-EP003970.

XX 06-APR-2000; 2000DE-01019058.

PR 07-APR-2000; 2000DE-01019173.

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX MPI; 2002-010922/01.

XX New nucleic acid derived from chemically treated metastasis genes, useful
PT for diagnosis of cancers by analysis of cytosine methylation, also for
PT treatment.

PS Claim 1; SEQ ID NO 79; 23pp + Sequence listing; English.

XX The present invention provides a number of human metastasis associated
CC genes which are modified by cytosine methylation. The sequences can be
CC used in the diagnosis and treatment of cancer. The present sequence is
CC one of the genes of the invention

XX SQ Sequence 6713 BP; 1676 A; 149 C; 1441 G; 3447 T; 0 U; 0 Other;

Query Match 4.7%; Score 54.2; DB 6; Length 6713;

Best Local Similarity 49.1%; Pred. No. 0.038;

Matches 143; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 16 AAAATCCAGATCATCTACTCATTTATGCACTTTCATCATGAAAACATCAAAACAGT 75

Db 1045 AAAATATACCTCCACTCCATTAAATTAATTATATAAAAAACAAAACAAATTACCGA 986

QY 76 CAAAGTAACAATAATCAAGTCAGATTCAGACACAAAGCCAGTAAGATGAAATTTTAA 135

Db 985 TACAAATTAATAATCAAAAAAACCTCATACATCTACTAAATTAATTAATTATTC 926

QY 136 GAACGCTCATGCTAAGCTGCGAAAATTAATCTTAATCAAAAACAGTAACACAGTAATT 195

Db 925 AACCACTATTAATAAACAAATAAATTCCTCAAAAAATAAACTAAACGATAATATA 866

QY 196 AGCAAAATCCGAGCAAAAACTCTCACCACCTCCGAAATTCAGCGTCTTCACTAAATTT 255

Db 865 ATCTAACAAATTTCTTAATAATATATATCTTAATAAAAAAAATCAATTAATAAAAAATA 806

QY 256 TCGAAAGGAATGATCAATACCAACCATTAACAAATAATACAAATTAATCAAAA 306

Db 805 TCTACATCCCATATTATTAACAACATTAATTCACAAATACTAAATATATAA 755

Search completed: August 14, 2005, 04:36:46
Job time : 731 secs

Db 181 TACACACAGTATTAGCAAAATCCGAGCAGAAAACCTCACCACCTCCGAATTACG 240
Qy 241 TCTTCACTAAAATTTTCGAAAGAAATCGATCAATACCAACCCATTACCAAAATACATTA 300
Db 241 TCTTCACTAAAATTTTCGAAAGAAATCGATCAATACCAACCCATTACCAAAATACATTA 300
Qy 301 TCAAAATGGCGGAATCGTACTCGAAACTTTGCTTCAAGTGGCAGAGAGAGAAAAGGA 360
Db 301 TCAAAATGGCGGAATCGTACTCGAAACTTTGCTTCAAGTGGCAGAGAGAGAAAAGGA 360
Qy 361 AGATCGTGAAGAAAGGGGTTTAGGTTAAGCTCAGACTCTATTGAGTAATAGGAGC 420
Db 361 AGATCGTGAAGAAAGGGGTTTAGGTTAAGCTCAGACTCTATTGAGTAATAGGAGC 420
Qy 421 GTGTCACATTTTCGTTTGAATGAACCTTGGGCTCAGTTAGGGCTATTAGATAT 480
Db 421 GTGTCACATTTTCGTTTGAATGAACCTTGGGCTCAGTTAGGGCTATTAGATAT 480
Qy 481 TGATGGGCTTTCTAGTAATACATTAATTAAGTTAGGGCTTAGTTAAATTAAGCCATGT 540
Db 481 TGATGGGCTTTCTAGTAATACATTAATTAAGTTAGGGCTTAGTTAAATTAAGCCATGT 540
Qy 541 TGGAAATATTGACACATGCTTGGCTACTAGTGTAAACATGCAACCGAAGAGTTGTCG 600
Db 541 TGGAAATATTGACACATGCTTGGCTACTAGTGTAAACATGCAACCGAAGAGTTGTCG 600
Qy 601 AGACAAGTCGACATATACATTAATGAATCAACACGCTAGTGTGCGCGCTCGCTCAT 660
Db 601 AGACAAGTCGACATATACATTAATGAATCAACACGCTAGTGTGCGCGCTCGCTCAT 660
Qy 661 GTGTCACTTGTCTCTGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTCA 720
Db 661 GTGTCACTTGTCTCTGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTCA 720
Qy 721 ATACAAATTTTGGGCTGTATCTTGCAAACTCTTGCAATCATCGCAATATACGTAACA 780
Db 721 ATACAAATTTTGGGCTGTATCTTGCAAACTCTTGCAATCATCGCAATATACGTAACA 780
Qy 781 CTGTGATCTAAATTTGTTGTGTTAAATGTTAAATTTAGATTCTATTTCTCGGTTTAAAG 840
Db 781 CTGTGATCTAAATTTGTTGTGTTAAATGTTAAATTTAGATTCTATTTCTCGGTTTAAAG 840
Qy 841 TGAATTTATATGATCATGTGTTAAACATTGTAAAGTAAGTAAATTAATTAATTAATTT 900
Db 841 TGAATTTATATGATCATGTGTTAAACATTGTAAAGTAAGTAAATTAATTAATTAATTT 900
Qy 901 AGTTGATGATAACGTAAGCAAAAATGAGATAGATACATTTGTTTGTGTAATTTT 960
Db 901 AGTTGATGATAACGTAAGCAAAAATGAGATAGATACATTTGTTTGTGTAATTTT 960
Qy 961 ACATAATGCGAGAGTAGCTACGCGCATGAGATCAAGAGACCTTGTGTAAGTCAAG 1020
Db 961 ACATAATGCGAGAGTAGCTACGCGCATGAGATCAAGAGACCTTGTGTAAGTCAAG 1020
Qy 1021 AGTGACGTGTAAAAGCTTGAAGTCCCCATGCAAACTTAATCTTAAGTGTCAA 1080
Db 1021 AGTGACGTGTAAAAGCTTGAAGTCCCCATGCAAACTTAATCTTAAGTGTCAA 1080
Qy 1081 ACCAGAGCTCACTGACATAATTAATCTCTCAAGTCCGCTTCTTATCATCT 1140
Db 1081 ACCAGAGCTCACTGACATAATTAATCTCTCAAGTCCGCTTCTTATCATCT 1140
Qy 1141 CTCACACAAACAAAAG 1158
Db 1141 CTCACACAAACAAAAG 1158

RESULT 2
AX707061 1164 bp DNA linear PAT 04-APR-2003
LOCUS AX707061
DEFINITION Sequence 13 from Patent WO03014347.
ACCESSION AX707061
VERSION AX707061.1 GI:29563372

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source
ORIGIN
Query Match 100.0%; Score 1158; DB 6; Length 1164;
Best Local Similarity 100.0%; Pred. No. 4.5e-228;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 421 GTGTCACATTTTCGTTTGAATGAACCTTGGGCTCAGCTTAATGAGTATTT 480
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QY 1141 CTCACAAACAAACAAAAG 1158
DB 1141 CTCACAAACAAACAAAAG 1158

RESULT 3

AX510242 1223 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 4937 from Patent WO0216655.
DEFINITION AX510242
ACCESSION AX510242.1 GI:23391479
VERSION
KEYWORDS
SOURCE
ORGANISM

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
AUTHORS Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE Strees-regulated genes of plants, transgenic plants containing
JOURNAL same, and methods of use
Patent: WO 0216655-A 4937 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)

FEATURES
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ORIGIN

Query Match 100.0%; Score 1158; DB 6; Length 1223;
Best Local Similarity 100.0%; Pred. No. 4, 5e-228;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CACAAACATACATCAAAATCCAGACTCAGATCTACTCAATTAATGCAATTCATCATGA 60
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QY 1141 CTCACAAACAAACAAAAG 1158
DB 1203 CTCACAAACAAACAAAAG 1220

RESULT 4

ATP2009 93695 bp DNA linear PLN 03-AUG-1999
LOCUS Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (BSSA
DEFINITION project).

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ACCESSION      AL021749
VERSION        AL021749.1
KEYWORDS       GI:2842474
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
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                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1
AUTHORS        Bevan, M., Rose, M., Hempel, S., Ertan, K.-D., Hobeisel, J.,
                Mewes, H.W., Mayer, K.F.X., Lemcke, K. and Schueller, C.
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 93695)
AUTHORS        EU Arabidopsis sequencing project.
TITLE          Direct Submission
JOURNAL        Submitted (30-JUN-1999) MIPS, at the Max-Planck-Institut fuer
                Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
                schueller@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
                Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
                Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                E-mail: michael.bevan@bbsrc.ac.uk
COMMENT        Information on performance of analysis and a more detailed
                annotation of this entry and other sequences of chromosomes 3, 4
                and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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Query Match 100.0%; Score 1158; DB 8; Length 93695;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 65141 CTCACAAACAAACAAAG 65158

RESULT 5
ATCHRIV69
LOCUS Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69.
DEFINITION Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69.
ACCESSION AL161573
VERSION AL161573.2 GI:7269705
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 36863)	exon	/number=2 complement(6286. .6456) /gene="AT4g28510"
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JOURNAL REFERENCE AUTHORS	Unpublished	exon	/number=3 complement(6575. .6691) /gene="AT4g28510"
JOURNAL REFERENCE AUTHORS	2 (bases 36754 to 80030) Lennard,N., Quail,M., Harris,B., Rajandream,M.A., Barrell,B.G., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Unpublished	intron	/number=4 complement(6692. .6935) /gene="AT4g28510"
JOURNAL REFERENCE AUTHORS	3 (bases 79912 to 177066) Brandt,P., Dose,S., Jarke,D., Scharfe,M., Schon,O., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Unpublished	exon	/number=4 complement(6936. .7106) /gene="AT4g28510"
JOURNAL REFERENCE AUTHORS	4 (bases 167625 to 197655) Hilbert,H., Braun,M., Holzer,E., Brandt,A., Duesterhoeft,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X. Unpublished	gene	/number=5 8330. .10351 /gene="AT4g28520"
JOURNAL REFERENCE AUTHORS	5 (bases 1 to 197655) EU Arabidopsis sequencing project. Direct Submission	CDS	join(8330. .8633,8759. .9183,9289. .9726,9944. .10351) /gene="AT4g28520"
COMMENT	Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mps.biochem.mpg.de, mayer@mps.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ this fragment has an overlap with ATCHRIV68 at the 5' end and an overlap with ATCHRIV70 at the 3' end. Location/Qualifiers		
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 T33017, R30004"
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Query Match 100.0%; Score 1158; DB 8; Length 197655;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-228;
 Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 7169 CACAAACATCACTCAAAATCCAGACTCACTCAATTCATTAATGCACTTCATGAA 7228
 QY 61 AACATCAAAACAGTCAAAAGTACAAATCAAGTTCAGTTCAGCAAAAGCAGTAAA 120
 DB 7229 AACATCAAAACAGTCAAAAGTACAAATCAAGTTCAGTTCAGCAAAAGCAGTAAA 7288
 QY 121 GATAGAAAATTTTAAACGACGCTCATGCTAAGCTGCCAAAATTAATCTTATCAAAAACAG 180
 DB 7289 GATAGAAAATTTTAAACGACGCTCATGCTAAGCTGCCAAAATTAATCTTATCAAAAACAG 7348
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 QY 301 TCAAAATGCGAGAAATCTGACTGAAACTTTGCTTCAAGTCGACAGAGAGAGAAAAGA 360

DB 7469 TCAAAATGCGAGAAATCTGACTGAAACTTTGCTTCAAGTCGACAGAGAGAAAAGA 7528
 QY 361 AATTCGTGAGAAAGGGGTTTGGGTTTAAAGTCAAGCTTCAATTCAGTAAATGGGAGC 420
 DB 7529 AATTCGTGAGAAAGGGGTTTGGGTTTAAAGTCAAGCTTCAATTCAGTAAATGGGAGC 7588
 QY 421 GTGTCACTTTTCCGTTTGGAAAATAAATTGGGCTCAGTTATGGGCTATTAGATATT 480
 DB 7589 GTGTCACTTTTCCGTTTGGAAAATAAATTGGGCTCAGTTATGGGCTATTAGATATT 7648
 QY 481 TGAATGGCTTTTCTAGTAAATTAACAATTAAGTTATGGGCTTAAATTAAGCCATGT 540
 DB 7649 TGAATGGCTTTTCTAGTAAATTAACAATTAAGTTATGGGCTTAAATTAAGCCATGT 7708
 QY 541 TGAATATTTTGAACATCTCTTGGCTACTAGTCAATCAATGCAACCGAAGAGTTGTG 600
 DB 7709 TGAATATTTTGAACATCTCTTGGCTACTAGTCAATCAATGCAACCGAAGAGTTGTG 7768
 QY 601 AGACAAGTGCAGCATATACAAATGATGCAAAACAGCCTAGTGGCGGCTCGCTCAT 660
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 QY 961 ACATATGCGAGAGAGTACGCGCATGAATCAAGAGACACTTCTGAGCTCACAG 1020
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 QY 1021 AGTACGTGTAAAAAAGCTTAGACTGAAGTCCCATGCAAACTTAATCTTACGTGCTCAA 1080
 DB 8189 AGTACGTGTAAAAAAGCTTAGACTGAAGTCCCATGCAAACTTAATCTTACGTGCTCAA 8248
 QY 1081 ACCAGAGCTCACTTGACAAATATTAATCTCTCTAGTCCCGTTCTTTCATCATCT 1140
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 QY 1141 CTCACACAAACAAAAG 1158
 DB 8309 CTCACACAAACAAAAG 8326

RESULT 6
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 LOCUS Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete cds.
 DEFINITION U66594
 ACCESSION U66594.1 GI:4097693
 VERSION
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 3054)

AUTHORS Sun, L. and Goodman, H.M.
TITLE Arabidopsis genes encoding prohibitin: importance for early development
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3054)
AUTHORS Sun, L., Nguyen, L. and Goodman, H.M.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1996) Molecular Biology Department, Massachusetts General Hospital, 50 Blossom St., Boston, MA 02114, USA
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ORIGIN
Query Match 98.9%; Score 1145.4; DB 8; Length 3054;
Best Local Similarity 99.8%; Pred. No. 1.6e-225;
Matches 1157; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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DB 1309 AACATCAAAAACAGTCAAAAGTAACAAATCAAGATTCAGCA CACAAACCAAGTAAA 1250
QY 121 GATAGAAAATTTAAGGAAGCTCATGCTTAAGCTGGCGAAAAAATCTTCTTAATCAAAACG 180
DB 1249 GATAGAAAATTTAAGGAAGCTCATGCTTAAGCTGGCGAAAAAATCTTCTTAATCAAAACG 1190
QY 181 TTAACAAGAGTAATAGCAAAAATCCGAGCAAAAATCTCAACCACTCCGAAATTCACG 240
DB 1189 TTAACAAGAGTAATAGCAAAAATCCGAGCAAAAATCTCAACCACTCCGAAATTCACG 1130
QY 241 TCTTCACTAAAATTTTCGAAAGAAATCGATCAATACCAACCCATTACACAAATATCATTA 300
DB 1129 TCTTCACTAAAATTTTCGAAAGAAATCGATCAATACCAACCCATTACACAAATATCATTA 1070
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QY 361 AGATCGTGAAGAAAGGGGTTTAGGGTTAAGCTCAGACTTCATTGAGAGTAATGGGACG 420
DB 1009 AGATCGTGAAGAAAGGGGTTTAGGGTTAAGCTCAGACTTCATTGAGAGTAATGGGACG 950
QY 421 GTGTCAATTTTCGTTTGAAGATGAATTTGGGCTCAGTTATGGGCTATTAGATAT 480
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QY 1140 TCTCACAACAAACAAAANG 1158
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RESULT 7
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LOCUS CQ875513
DEFINITION Sequence 6 from Patent WO2004076616.
ACCESSION CQ875513
VERSION CQ875513.1 GI:52748477
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (chale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 Broekaert, W. and Hatzfeld, Y.
AUTHORS Arabidopsis promoters
TITLE Patent: WO 2004076616-A 6 10-SEP-2004;
JOURNAL CropDesign N.V. (BB)
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.9e-209;

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QY 466 GGGCTTTCTAGTAATATCAATATATATATATATATATATATATATATATATATATAT 545
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QY 1085 CGAGCTCACTTGAACAT 1144
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QY 1145 CAACAAACAAAAG 1158
DB 971 CAACAAACAAAAG 984

RESULT 9
BX296428/c 329 bp DNA linear STS 10-JUN-2003
LOCUS Arabidopsis thaliana transposon insertion STS SM_3.33744, sequence
DEFINITION tagged site.
ACCESSION BX296428
VERSION BX296428.1 GI:29170295

KEYWORDS STS, STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,
Murphy,G., Langham,S., Legrys,C., Jones,J.D.G. and Bevan,M.
Unpublished
2 (bases 1 to 329)
REFERENCE
AUTHORS Clarke,J.H.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2003) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
COMMENT AR denotes an activation tag dissociation transposon. Gr a gene
single line, ET an enhancer trap dissociation transposon within a
trip dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SW a defective suppressor mutator
transposon, _3 denotes a sequence derived from the 3' end of the
transposon, _5 denotes a sequence derived from the 5' end of the
transposon BSRG GARNet, ATIS project
On-line seed stock requests: <http://nasc.nott.ac.uk/NASCstock>
code: DEAD.

FEATURES
Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.ee-44;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 953 GTATTTTGAATATGCGAGAGTGAAGCTACGCGCATGAAGATCAAGAGACCTTGCTCGA 1012
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QY 1013 GCTCAGAGTGAAGCTGTAAAAAGCTTGACTGAAGTCCCATGCAAACTTAATCTTACG 1072
DB 185 GCTCAGAGTGAAGCTGTAAAAAGCTTGACTGAAGTCCCATGCAAACTTAATCTTACG 126
QY 1073 TGGCTCAACACGAGCTCAGCTGCAATATATTAATCTCTCTPAAGTCCGTTCTCTTC 1132
DB 125 TGGCTCAACACGAGCTCAGCTGCAATATATTAATCTCTCTPAAGTCCGTTCTCTTC 66
QY 1133 ATCCATCTCTCAACAAACAAAAG 1158
DB 65 ATCCATCTCTCAACAAACAAAAG 40

RESULT 10
BNCRU1
LOCUS B. napus cru1 gene for cruciferin subunit.
DEFINITION X62120 S48084
ACCESSION X62120.1 GI:117800
VERSION 125 storage protein; cruciferin.
KEYWORDS Brassica napus (rape)
SOURCE Brassica napus
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

	REFERENCE
AUTHORS	1 (bases 1 to 4105)
TITLE	Rodin,J., Sjodahl,S., Josefsson,L.G. and Rask,L.
JOURNAL	Characterization of a Brassica napus gene encoding a cruciferin
MEDLINE	Subunit: estimation of sizes of cruciferin gene families
PUBMED	Plant Mol. Biol. 20 (3), 559-563 (1992)
REFERENCE	1421158
AUTHORS	2 (bases 1 to 4105)
TITLE	Rodin,J.
JOURNAL	Direct Submission
SOURCE	Submitted (09-SEP-1991) J. Rodin, Dept of Cell Research, Swedish University of Agricultural Sc., Box 7055, S-75007 Uppsala, SWEDEN
FEATURES	Location/Qualifiers
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misc_feature	/db_xref="taxon:3708"
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	1189..1194
	/gene="crui"
	1220..
	/note="CAP site"
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	GQQGQGCGGGGFRDMHCKVHRHGDIATTASSHRYTGTGPVITICTLIANY
	QNQLDRNRTRVLGNPFQGSQQGQQQQNMLSGFDPQVLAQALKIDVRVAELQNC
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	/gene="crui"
	/number=3
intron	2606..2870
	/gene="crui"
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polyA_signal	3429..3434
	/gene="crui"
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Query Match	17.2%; Score 198.8; DB 8; Length 4105;
Best Local Similarity	66.0%; Pred. No. 7,9e-31;
Matches 409; Conservative	0; Mismatches 177; Indels 34; Gaps 77;

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RHPRPPOSNDNGLEETICSMRTHENTIDPRADYVKNLGRVSVNSYLPILQYI
RISATRGILQGNAMVLPKYNNMANEILYCTGQARIQVNDNGOVLDQOVKGOLV
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intron
1471..1567
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2272..2676
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Best Local Similarity 63.7%; Pred. No. 3.5e-27;
Matches 392; Conservative 0; Mismatches 180; Indels 43; Gaps 6;
574 GCTAAACATGCAACGGAAGTTGCGAGCAAGTCGCGCATATCAATGATCAACA 633
135 GCTAAACATGCAACGGAAGTTGCGAGCAAGTCGCGCATATCAATGATCAACA 194
634 GCGCTAGTGGCGGCTGCTGCTCATGTCACCTGTTCTGTTTCTTTTAAATT 693
195 CTCGGAGATGTCGCGGCTGCTGCTCATGTCACCTGTTCTGTTTCTTTTAAATT 252
694 TTCATAGTCTTTTGTTCATATCAATCAAAATTTTGGCTGATCTTGCAAACTCTT 753
253 GGTAAAC-----TTTTTTTTTGGAAACAAGTTTGGTGTATCTCCAAACTGTT 302
754 CGATCATATCGCCA-----ATATACGTGAACACTGGTATCTAATTTGTTGTTAAT 807
303 CGATTGCAAGCGCTAGATATTTTAAATCCTGACACATGATATTAATTTGTTAAT 362
808 GTTAATTTAGATTTCATTCGCGTTTAAAGTAAATGATATATATCATGTTAAACA 867
363 GTCAAAAAAGTAGATTCCTCATATGACCATATCTCGTTTAACTCACTATATGATTAA 422
868 TTGTAGTAGATGATATTA-----ATGATTAATTTAGTTGA 906
423 ATGAATTTAAGCGACTAATAATGATTACTCAATCAACAGAGTTGCTATATGATATA 482
907 TGGATTAAGCTGAAGCAAAAAATGAGATAGATCAATTTG-ATTTTGTGATTTTGA 965
483 GTGATTAACATGAAGCAAAAAATGAGATAGATCAATTTGATTTTGTGTTGAGTA 542

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QY 966 TCCGAGAGTGAAGTACCGGCGATGAAGATCAAGAGACCTTGCTGAGCTCAAGATGA 1025
DB 543 TCCGGAGATTGTGCTACCGGCGATGAAGATGAAGACCTTGCTGAGCTCAAGATGA 602
QY 1026 CCGTAAAAAGCTTGAAGTGAAGTCCCATGCAACCTTAATCTTACGTGGCTCAACCGAC 1085
DB 603 CCGTAAAAAGCTTGAAGTGAAGTCCCATGCAACCTTAATCTTACGTGGCTCAACCGAC 662
QY 1086 GAGCTCACTGACATATTAATCTGCTAAGT---CCGTTGCTTCAATCAATCTCT 1142
DB 663 CATGCTCACTCCATATATTAATCCCTTACATGCTCAATCTTCTTCAATCAATCTCT 722
QY 1143 CACAACAAACAAAA 1157
DB 723 CACAACAAACAAAA 737
RESULT 13
BX545778 150 bp DNA linear STS 23-JUN-2003
LOCUS BX545778/c
DEFINITION Arabidopsis thaliana transposon insertion STS SM_3.36286, sequence tagged site.
ACCESSION BX545778
VERSION BX545778.1 GI:32169011
KEYWORDS STS, STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1 Clarke,J.H., Bowles,B., Carter,J.J., Hart,D., McCullagh,B., Walsh,S., Langham,S., Legrys,C., Jones,J.D.G. and Bevan,M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 150)
AUTHORS Clarke,J.H.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2003) Clarke J.H., John Innes Centre, Colney lane, Norwich, NR4 7UJ, UK
COMMENT
AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon. _5 denotes a sequence derived from the 5' end of the transposon BBSRC GARNET, AIT's project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock code: N122997.
FEATURES
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/mol_type="genomic DNA"
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/db_xref="taxon:3702"
/cloned="AL021749"
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1..150
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Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
895 AAATTAGTGAATGATACGTAAGCAAAAAATGATAGATGATGATTTGTTGCT 954
DB 150 AAATTAGTGAATGATACGTAAGCAAAAAATGATAGATGATGATTTGTTGCT 91
QY 955 ATTTTGAATATGCGGAGAGTGAAGTACCGGATGAAGATCAAGAGACATTGCTCGAC 1014
DB 90 ATTTTGAATATGCGGAGAGTGAAGTACCGGATGAAGATCAAGAGACATTGCTCGAC 31
QY 1015 TCACAGAGTGAAGTGAAGGCTTAAAGCTTAACT 1044

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Db	30	TCAACAGTGCCTGTATAAAGCTTAGACT	1
RESULT 14			
LOCUS	BX296260/c	180 bp	DNA linear STS 10-JUN-2003
DEFINITION	Arabidopsis thaliana transposon insertion STS SM_3.23228, sequence tagged site.		
ACCESSION	BX296260		
VERSION	BX296260.1	GI:29170125	
KEYWORDS	STS; STS, sequence tagged site.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	1		
JOURNAL	Clarke,J.H., Bowles,B., Cater,J., Hart,D., McCullagh,B., Murphy,G., Langham,S., Legrys,C., Jones,J.D.G. and Bevan,M.		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 180)		
TITLE	Clarke,J.H.		
JOURNAL	Direct Submission		
COMMENT	Submitted (24-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK		
	At denotes an activation tag dissociation transposon within a single line, Et an enhancer trap dissociation transposon, Gt a genome trap dissociation transposon, Mt a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon, _5 denotes a sequence derived from the 5' end of the transposon, BBSRC GARNET, ARIS project		
	On-line seed stock requests: http://nasc.nott.ac.uk/NASC_stock_code/		
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	Query Match	10.3%	Score 119; DB 11; Length 180;
	Best Local Similarity	100.0%;	Pred. NO. 2.9e-14;
	Matches 119; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
QY	893 ATAAATTAGTTGATGATGAATACGTCGACCAAAAAATGAGATAGATACATTTGATTTTTC	952	
Db	119 ATAAATTAGTTGATGATGAATACGTCGACCAAAAAATGAGATAGATACATTTGATTTTTC	60	
QY	953 GTATTTTGACATATGCGGAGAGTGAGCTACGCGCATGAAGATCAAGACACTTGCTCG	1011	
Db	59 GTATTTTGACATATGCGGAGAGTGAGCTACGCGCATGAAGATCAAGACACTTGCTCG	1	
RESULT 15			
LOCUS	BX296270/c	205 bp	DNA linear STS 10-JUN-2003
DEFINITION	Arabidopsis thaliana transposon insertion STS SM_3.23221, sequence tagged site.		
ACCESSION	BX296270		
VERSION	BX296270.1	GI:29170135	
KEYWORDS	STS; STS, sequence tagged site.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		

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REFERENCE
AUTHORS      Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B.,
              Murphy,G., Langham,S., Legrys,C., Jones,J.D.G. and Bevan,M.
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 205)
AUTHORS      Clarke,J.H.
TITLE        Direct Submission
JOURNAL      Submitted (24-MAR-2003) Clarke J.H., John Innes Centre, Colney
              Lane, Norwich, NR4 7UJ, UK
COMMENT      AT denotes an activation tag dissociation transposon within a
              single line, ET an enhancer trap dissociation transposon, GT a gene
              trap dissociation transposon, MT a mis-expression enhancer trap
              dissociation transposon, SM a defective suppressor mutator
              transposon, _3 denotes a sequence derived from the 3' end of the
              transposon, _5 denotes a sequence derived from the 5' end of the
              transposon BBSRC GARNet, AIT's project
              On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
              code: N110901.
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STS          1..205
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Best Local Similarity 100.0%; Pred.No.2.9e-14;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      893 ATAAATTAGTGTGATGATAACGTGAAGCAAAAATGAGATAGATACATTGGATTGGTC 952
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QY      953 GTAATTTGACATATGCGGAGAGTAGTGACTAACGCGCATGGAATCAAGAAGACACTTGGCTCG 1011
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Db      59 GTAATTTGACATATGCGGAGAGTAGTGACTAACGCGCATGGAATCAAGAAGACACTTGGCTCG 1

Search completed: August 14, 2005, 06:06:56
Job time : 5406 secs

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: FILE REFERENCE: PU3480US
: CURRENT APPLICATION NUMBER: US/09/710,279
: CURRENT FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: 60/164,258
: PRIOR FILING DATE: 1999-11-09
: NUMBER OF SEQ ID NOS: 4472
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1601
: LENGTH: 694
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: synthetic
: OTHER INFORMATION: nucleic acid sequence
: US-09-710-279-1601

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Best Local Similarity	51.8%	Pred. No. 0.0013		
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 Db 246 ATTACTCTGTTTAATTAAGATATATCAATTTCTAGATGGCGCTACTACTTTTGA 305

Oy 757 TCAATCGCCAAATACGTGAACACTGGATCTAATTTGTTGGTTAATTTGTTAAATTT 816
 Db 306 TTTCACGCTACTATTTTAAATGAAGAATCAATTAACTCCATTTTACAAACAATTAAATAT 365

Oy 817 AGATTCTCTCCGATTAAAGTGAATATATATCATGTAAACATTGTAAGTA 876
 Db 366 TGCCTATACCACCTTTAAAAAGTGAATATAGTATCTCGGATTTTATATATGGATTAA 425

Qy	877	AGATGATATATAAATGATAAATTTAGTTGATGATTAACGGAGCAA	924
Db	426	AGAAATGAAATCAAAAGATGATCAAAATCAAGTTGTGTGTCCATCAA	473

RESULT 3
US-09-710-279-3860
Serial# 3860 Production # 00710070

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? Patent No.6703492
? GENERAL INFORMATION:
? APPLICANT: KIMMERLY, WILLIAM JOHN
? TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
? FILE REFERENCE: P034800S
? CURRENT APPLICATION NUMBER: US/09/710,279
? CURRENT FILING DATE: 2000-11-09
? PRIOR APPLICATION NUMBER: 60/164,258
? PRIOR FILING DATE: 1999-11-09
? NUMBER OF SEQ ID NOS: 4472
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 3860
? LENGTH: 3028
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: synthetic
? OTHER INFORMATION: nucleic acid sequence
? US-09-710-279-3860

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Nb 2580 ATTACCTGTGTTAATTTTAAAGATATATCATTTCTAGATGGCGCTACTACTTTTGA 2639

Qy 757 TCAATATCGCCAAATATACGCGAACACTGGGATCTTAATTTGTGGTTAATTTGTTAAATTT 816
Db 2640 TTTCACGCTACTATTTTAAATGAAGTCATTAACTCCATTTTACAAACATTAATAATTT 2699

817 AGATTCTATTCTCCGGTTTAAAGTGAATTATATGTATCATGGTTAAACATTGTAAGTA 876

Db	2700	TGCTTATACCACCTCTTTAAAAAGTAATAGATCTCGAGATTTTATATATTGGATTAA	2759
Oy	877	AGATGATATATTAATGATTAATTAGTTGGATGCAACGTGACCAAA	924
Db	2760	AGAAATGATCAAAAGATGATCAAAATCAAGTTGTGTTCATCAAA	2807

RESULT 4
US-09-710-279-4227

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; GENERAL INFORMATION:
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; APPLICANT: KIMMERLY, WILLIAM JOHN

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CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09

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; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: DNA
; ORGANISM: Artificial Sequence
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OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4227

Best Local Similarity 51.8%; Pred. No. 0.0022;
Matches 118; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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Db
2749 TTCCACGCTACTATTTTAAAGAAAGTCATTAACTCATTTTTACACAATTAAATAT 2808

Db 2809 TGCCTATACCACTTTAAAAAGTAATATAGTATCTCGATTTTTATAATTGCATTAA 2868

Db
2869 AGAAATGAATCAAAAGATGATCAAAATCAAGTTGTGTTCATCAA 2916

RESULTS 5
US-09-710-279-759
Communication inc/00710270

APPLICANT: KIMBERLY, WILLIAM JOHN
SITE OF INTEREST: CADDYWOOD VICTORIA LODGE AND PROTECTING

;
 ; CURRENT APPLICATION NUMBER: US/09/110,219
 ;
 ; CURRENT FILING DATE: 2000-11-09
 ;
 ; PRIOR APPLICATION NUMBER: 20/164,358

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; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 44/2
; SEQ ID NO. 750

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1 TYPE: DNA
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3 ORGANISM: Artificial Sequence
4
5 PROTEIN:

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OTHER INFORMATION: nucleic acid sequence

US-09-710-279-759

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Best Local Similarity 51.8%; Pred. No. 0.003;
Matches 118; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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DB 246 ATTAAGTCTTTTAAATTTAAAGATATATCAATTTTCAATGGCGCTACTACTTTTGA 305
QY 757 TCATATGCCAATATACGGAACACTGGATTAATTTGTGTATTTGTTAAATTT 816
DB 306 TTTCCAGCTACTATTTTAAAGAAATCAATTTTCACTTTTCAATTAATATAT 365
QY 817 AGATTCATTCCTCGGTTAAAGAAATATATATATATATATATATATATATATATAT 876
DB 366 TGTCTATACCACTCTTTTAAAGATATATATATATATATATATATATATATATAT 425
QY 877 AGATGAT 924
DB 426 AGAAATGATCAAAAGATGATCAAAATCAATGTTGTGTCTCAAA 473

RESULT 6
US-08-894-731-2
Sequence 2, Application US/08894731
Patent No. 6084089

GENERAL INFORMATION:
APPLICANT: MINE, Toshiki
APPLICANT: OHYAMA, Akio
APPLICANT: HIYOSHI, Toru
APPLICANT: KASAKURA, Keisuke
TITLE OF INVENTION: COLD-INDUCIBLE PROMOTER SEQUENCE
FILE REFERENCE: 760-234P
CURRENT APPLICATION NUMBER: US/08/894, 731
CURRENT FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 4140
TYPE: DNA
ORGANISM: Solanum tuberosum
US-08-894-731-2

Query Match 4.3%; Score 49.8; DB 3; Length 4140;
Best Local Similarity 48.1%; Pred. No. 0.009;
Matches 141; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

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QY 729 TTTGGCTGTATCTTCAAACTCTTGATCATATTCGCAATATATAGTGAACACTGTGTAT 788
DB 1099 TATTCGTTGTTTATATTAACGTTTGTGTATCAACAAATCATATATATTTGTT 1158
QY 789 CTAATTTGTGTATTTTATTTTAAATTTTCAATTTCTATCTCCGTTTAAAGTATAT 848
DB 1159 GTAATATGATGCTCGCAATTAAGTTTCTTTTAAATTTTGTATTTTGTATTTGTC 1218
QY 849 ATGTATCATGTTTAAATATTTGTAATATATATATATATATATATATATATATATAT 908
DB 1219 ATGTCAATTTTCAAAATTTTATCAATATGTTCTTTTGTATGTATGTGTATACCA 1278
QY 909 GATTAACGTAAGCAAAATATGATATATATATATATATATATATATATATATATAT 961
DB 1279 TACAACCTTGAATTAATTTTCAAGTATATATTTTGTATTTTGTATATATATAT 1331

RESULT 7
US-09-601-198-51
Sequence 51, Application US/09601198
Patent No. 6531583

GENERAL INFORMATION:
APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellison Y.
APPLICANT: Glase, Jennifer S.
APPLICANT: Glase, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
FILE REFERENCE: UAB-13452/22

QY 693 TTTCAATGCTTTTGTTCATTCATACAAATTTTGGCTGTATCTTGCAACTCT 752
DB 385 TGTATATCTCTGTTTGGAGCAAGTTTAAATTTATTTAGATTTTAAATTAATCTT 444
QY 753 TCGATCATATCCCAATATATAGTGAACACTGTGTATTTTGTGTATTTGTTAA 812
DB 445 TTCATATCTTTTAAAGTCTTGAATGTTTGAATGATTTGATTTTATTTATTTGATC 504
QY 813 ATTTAGATTTCTTCCGTTTAAAGTAAATATATATATATATATATATATATATAT 872
DB 505 GTTTTCAATTTTAAATTTCAATTTTAAATCTTTTAAATGTTTAAATGATTTTAAAT 564
QY 873 AGTAAGAT 932
DB 565 ATTAATTTTGTAAATTTGATTAATGTTTGTATTTTAAATTTTAAATCAACATCAAT 624
QY 933 TAGATCATTTGATTTTGTGTATTTTGAATATGACATATGAC 968
DB 625 TTGTGAATTAAGCTTTTGAATTTTATTTTATTTATTTATTC 660

Query Match 4.2%; Score 48.8; DB 4; Length 1851;
Best Local Similarity 48.6%; Pred. No. 0.012;
Matches 134; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

US-09-806-708B-22
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806, 708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)-(1141)
OTHER INFORMATION: consensus sequence of A.c., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

Query Match 4.2%; Score 48.6; DB 4; Length 1141;
Best Local Similarity 10.2%; Pred. No. 0.012;

[illegible]

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RESULT 11
US-09-949-016-156535/c
; Sequence 156535, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01107
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156535
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-156535

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[illegible]

```

: Sequence 22, Application US/09806708B
: Patent No. 6784342
: GENERAL INFORMATION:
: APPLICANT: The University of British Columbia
: TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
: FILE REFERENCE: 4810-58741
: CURRENT APPLICATION NUMBER: US/09/806,708B
: CURRENT FILING DATE: 2001-04-03
: PRIOR APPLICATION NUMBER: US 60/147,133
: PRIOR FILING DATE: 1999-08-04
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 22
: LENGTH: 1141
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: NAME/KEY: promoter
: LOCATION: (1)..(1141)
: OTHER INFORMATION: consensus sequence of A.c., L.a., and B.n. PAEI promoter
US-09-806-708B-22

Query Match          4.1%; Score 47.4; DB 4; Length 1141;
Best Local Similarity 9.9%; Pred. No. 0.023;
Matches      88; Conservative 326; Mismatches 469; Indels 2; Gaps 1;

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Query Match	Similarity	4.1%;	Score 47.4;	DB 4;	Length 1141;
Best Local	Similarity	9.9%;	Pred. 0.023;		
Matches	86;	Conservative	326;	Mismatches	465;
				Indels	2;
				Gaps	1
Qy	7	CATACACTCAAAATCCAGACTCATCATCTACTCAATTAATGACATTCATCATGAAACATC	66		
Db	961	MAAATACTGMMADTAGKCKCNCNNNNNNNTTIDVRRMAKACNNNNNNNAAYTACYNRAATNNKK	902s		
Qy	67	AAAAACGTCMAAGTAAACAAATCAAGTCAGATTGACAGCAAAAGCCAGTAAAGATGAA	122s		
Db	901	ATATMMKWTGASKRTTRHTTCTCRRTEKYNNNNNNAATVYVYHHAARRMMAWMTTRNN	842s		
Qy	127	AAATTTAGCAAGCGCTCAAGCTCAGCGCAAAATACTCTCTATGCAAAACAGTAAACA	186s		
Db	841	NNNNNNNACRNTRTTMMBKHSKCNNNNNNNNNNNNTTCHYTANABCEYRANNNNA	782s		
Qy	187	CGAGTAATTAGCAAAATCCAGACAGAAAATCTCACCCACTCCGAAATTCACGCTTTCA	246s		
Db	781	ARAAATCCNNYMAAAVTTHTTIDWCYKTMNTTYYWIDMTTMBTTTRNNMTSTNNNNNNNN	722s		
Qy	247	CTAAAAATTTCCAAAGGAATGCATGATAATCAACACCCATTAACAAAAATACATAATCAAA	306s		
Db	721	MMACTNNNNNNNNKAYAAATATNNMCWNNNNNTDARTNNNTYVMBRRMMTNTKTRMYSTTR	662s		
Qy	307	TGGCGAGATCGTACCTGSGAAACCTTGCTTCAAGTCGAGACAGAGAAAAGCAAGATCG	366s		
Db	661	HHYTTGTTNNNNNNNNNNNNNNNNNSCCTTRMTTMRWTGKSGMVRKKVKARDTTCYYVD	602s		
Qy	367	TGGAGAAAGGGGTTTAGGGTTTAAGCTCAGACTTCTATTGAGTAAATGGGACGGTCA	426s		
Db	601	VMAADSVVMMYAAWMBRCDTVTYRNTYCKSYAHSHVWVSSNNAMYYRYASANNSSMARWT	542s		
Qy	427	CATTTTCGTTTGGAAATGAACCTTGAGCTCAGCTTATGGGCTATTAGATATTGATCG	486s		
Db	541	TRNNMMMSGBVMBRMAGTMMWMMHNNNNNTDTRYYWWWKRAVBTYYDVSCKAASKWRG	482s		
Qy	487	GCCTTCTAGTAATCAATTAAGTATTATGGGCTTAGTTAAATPAACCAATGTTGGAA	546s		
Db	481	NNRPAKMMMAAANDGADHWTTMGNNITMMRRAMKMMMAHCRAYACNNNNNNPACV	4222s		
Qy	547	TATTTGACACATGTCTTGCTACTAGTCTAAACATGCAACGGAACAGTTGTCGAGCAA	606s		
Db	421	WHKHKMWRWTYKMMKCAACNNNNBVAMTMRAYAMMYUSDITNDIDMMNTSDMBVHNYTVD	352s		
Qy	607	GTGCGACATPAACATGATCAAAACGCTAGTGTGCGCGCTCTGCGCTCATGTGTCA	666s		
Db	361	YTMRRAMNNNNNNNNBRCKTTSMMWMDHNNHTCTYGNNTTGSAYBVAAASMMMAAGASNB	3020s		
Qy	667	CCGTGTTTCCGTTTTTTTTTAATTTCAATTAAGTCTTTTGTGTTATGTTCAATGAA	726s		
Db	301	VYNNCWRATYTGKTL-MTNNNNNNKAAVYATKTVAACNNRYUDTAVMVBKRNKYCTVA	2444s		

Qy 727 ATTTTGCTGATCTTCAAACTCTTCATCATATCCCAATATACGTGAACCTGGTG 786
Db 243 YBMYBYMYGKHMBWMBABRSNNMMWVKCRKNYVMYSHYHARBYKMAHVAVCNNMW 184
Qy 787 ATCTAATTTGTTGTTTAATTTGTAATTTAGATTCTTCCCGTTTAAAGTAATT 846
Db 183 KDRMAHHHCATNNNNMMWYAVMMHMKKGAAWTNNKTAHRDHBHVKTYWYWRDY 124
Qy 847 ATATGATCATGTTAAACATTTGTAAGATGATGATAATAAT 891
Db 123 WCACMMANAKAKVRITAMKHMVYTRIVYSANNTGVRMMMRKCMW 79

RESULT 13
US-09-902-540-1357/c

/ Sequence 1357, Application US/09902540
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 1357
/ LENGTH: 612
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(612)
/ OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match 4.0%; Score 46; DB 4; Length 612;

Best Local Similarity 51.2%; Pred. No. 0.043; Matches 106; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 669 TTGTTCCGCTTTTATTTTATTTTCAATAGTCTTTGTTATCTTCAATACAAT 728
Db 539 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
Qy 729 TTTTGGCTGATCTTGCAACTCTTCATCATATGCCAATATACGTGAACCTGGTAT 788
Db 479 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 420
Qy 789 CTAATTTGTTGTTAATTTGTAATTTAGATCTTATCTCCGTTTAAAGTAAAT 848
Db 419 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 360
Qy 849 ATGATCATGTTAAACATTTGTAAGT 875
Db 359 ATTATTTTATTTTATTTTATTTTATTT 333

RESULT 14
US-08-232-463-14/c

/ Sequence 14, Application US/08232463
/ Patent No. 5670367
/ GENERAL INFORMATION:
/ APPLICANT: DORNER, F.
/ APPLICANT: SCHEIFLINGER, F.
/ APPLICANT: FALKNER, F. G.
/ TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner

/ STREET: 1800 Diagonal Road, Suite 500
/ CITY: Alexandria
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 22313-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/232,463
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/935,313
/ FILING DATE:
/ APPLICATION NUMBER: EP 91 114 300.6
/ FILING DATE: 26-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 30472/114 IMMU
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149

/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7218 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: pTZgpt-F18
US-08-232-463-14

Query Match 4.0%; Score 45.8; DB 1; Length 7218;

Best Local Similarity 2.1%; Pred. No. 0.12; Matches 8; Conservative 217; Mismatches 154; Indels 0; Gaps 0;

Qy 58 GAAACATCAAAAACGTCGAAGTAACAAATCAAGTACGACGACAAAGCCAGT 117
Db 1431 RRR 1372
Qy 118 AAGATAGAAATTTAAGACGCTCATGCTAAGCTGCGCAAAATCTCTAATCAAA 177
Db 1371 RRR 1312
Qy 178 CAGTAACAGAGTAATTAAGCAAAATCGAGAGAAAATCTCACCACTCCGAATTC 237
Db 1311 RRR 1252
Qy 238 ACGTCTCACTAAATTTTCAAAAGAAATCATATCAACCACTTACCAAAATCA 297
Db 1251 RRR 1192
Qy 298 TAATCAAAATGCGGAATCGAATCTTGGAATCTTCAAGTCGAGAGAGAGAAA 357
Db 1191 RRR 1132
Qy 358 GGAAGATCGTGAAGAGGTTAAGGTTTAAGCTCACTGACTTATTTGAGTAATGG 417
Db 1131 RRR 1072
Qy 418 ACGGTGCATTTTCCGT 436
Db 1071 RRRRATCGAAGCTCCT 1053

RESULT 15

US-09-949-016-14004
/ Sequence 14004, Application US/09949016

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 14004
; LENGTH: 4529
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14004

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Query Match          3.9%; Score 45.6; DB 4; Length 4529;
Best Local Similarity 46.3%; Pred. No. 0.11;
Matches 150; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

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QY 670 TGTTCCTGCTTTTATTTTCAATGATCTTTGTTTATCTTCAATGAAAT 729
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1561 TATTTTATGATATATATATATATATATATATATATATATATATAT 1620
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 730 TTGGCTGATCTTGAACCTCTCGATCATATCGCAATATACGTGAACACTG 789
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1621 TTATATATTTTATGATATATATATATATATATATATATATATATAT 1680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 790 TAATTTTGTGTAATTTGTAATTTAGATTTCTATCTCCGTTTAAAGTA 849
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1681 ATATATTTATATATATGATATATATATATATATATATATATATAT 1740
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 850 TGTATCATGTTAAACATTTGTAAGATGATATATATATATATATATAT 909
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1741 TATATATATTTATATATATTTTATGATATATATATATATATATAT 1800
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QY 910 ATTAACGTGAAGCAAAAAATGAGATAGATACATTTGTTGCTATTTTGA 969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1801 ATATTTTATATATATTTATATATATATATATATATATATATATAT 1860
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 970 GAGAGTGAGCTACGCCATGAGA 993
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1861 TAGAGATATATGTAATATGACATA 1884
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Search completed: August 14, 2005, 02:10:22
 Job time : 238 secs

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Db 1 CACAAACATACCTGAAAAATCCAGACTCAGATCTACTGATTAATGCAACTTCATCATGAA 60
QY 61 AACATCAAAAAAGTCAAAAGTAACAAAAATCAAGTGAATTCAGACACAAAGCCAGTAA 120
Db 61 AACATCAAAAAAGTCAAAAGTAACAAAAATCAAGTGAATTCAGACACAAAGCCAGTAA 120
QY 121 GATGAAAAATTTAAGAAAGCTGATGCTAAGCTGGCGAAAAATCTTCTTAATCAAAACAG 180
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QY 121 GATGAAAAATTTAAGAAAGCTGATGCTAAGCTGGCGAAAAATCTTCTTAATCAAAACAG 180
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QY 181 TAACACGAGTAATAGCAAAAAATCCGAGCAGAAAAATCTCAACCCAGCTCCGAAATTCACG 240
Db 181 TAACACGAGTAATAGCAAAAAATCCGAGCAGAAAAATCTCAACCCAGCTCCGAAATTCACG 240
QY 241 TCTTCACTAAATTTTCGAAAGAAATCGATCAATAACAAACCATTTACACAAATACATTA 300
Db 241 TCTTCACTAAATTTTCGAAAGAAATCGATCAATAACAAACCATTTACACAAATACATTA 300
QY 301 TCAAAATGCGGAGAAATCTGTAAGCTGAAACCTTGTCAAGTCGACAGAGAGAGAAAAAG 360
Db 301 TCAAAATGCGGAGAAATCTGTAAGCTGAAACCTTGTCAAGTCGACAGAGAGAGAAAAAG 360
QY 361 AGATCGTGAAGAAAGGGGTTTAAAGCTGAGACTTCTATTTGAGTAATGGAG 420
Db 361 AGATCGTGAAGAAAGGGGTTTAAAGCTGAGACTTCTATTTGAGTAATGGAG 420
QY 421 GTGTCACTTTTCGTTTGGAAATGAACTTGGGCTCAGCTTATGGGCTATTAGATAT 480
Db 421 GTGTCACTTTTCGTTTGGAAATGAACTTGGGCTCAGCTTATGGGCTATTAGATAT 480
QY 481 TGATGGGCTTTCTAGTAATACAAATTAAGTTATGGGCTTAAATTAATGAGCCATGT 540
Db 481 TGATGGGCTTTCTAGTAATACAAATTAAGTTATGGGCTTAAATTAATGAGCCATGT 540
QY 541 TGAATAATTTTGAACATGCTTTGGCTACTAGTCTAAACATGACAGCAAGCAAGTTGTCG 600
Db 541 TGAATAATTTTGAACATGCTTTGGCTACTAGTCTAAACATGACAGCAAGCAAGTTGTCG 600
QY 601 AGACAAATTTTGAACATGCTTTGGCTACTAGTCTAAACATGACAGCAAGCAAGTTGTCG 600
Db 601 AGACAAATTTTGAACATGCTTTGGCTACTAGTCTAAACATGACAGCAAGCAAGTTGTCG 600
QY 661 AGACAAATTTTGAACATGCTTTGGCTACTAGTCTAAACATGACAGCAAGCAAGTTGTCG 660
Db 661 AGACAAATTTTGAACATGCTTTGGCTACTAGTCTAAACATGACAGCAAGCAAGTTGTCG 660
QY 721 ATACAAATTTTGGCTGATATGCAAACTCTTGCATCATATGCGCAATATATGCGAACA 780
Db 721 ATACAAATTTTGGCTGATATGCAAACTCTTGCATCATATGCGCAATATATGCGAACA 780
QY 781 CTGATGATCTAATTTGTGTGTTAAATGTTAAATTTAGATTTCTATCTCCGGTTTAAAG 840
Db 781 CTGATGATCTAATTTGTGTGTTAAATGTTAAATTTAGATTTCTATCTCCGGTTTAAAG 840
QY 841 TGAATTAATGATATGATGTTAAACATTTGTAAGTAAGTGAATTAATAATGATTAATTT 900
Db 841 TGAATTAATGATATGATGTTAAACATTTGTAAGTAAGTGAATTAATAATGATTAATTT 900
QY 901 AGTTGATGATTAAGTGAAGCAAAAAATGAGATGATATGATTAATTTGTCGTAATTTTG 960
Db 901 AGTTGATGATTAAGTGAAGCAAAAAATGAGATGATATGATTAATTTGTCGTAATTTTG 960
QY 961 ACATATGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
Db 961 ACATATGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
QY 1021 AGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
Db 1021 AGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
QY 1081 ACCAGAGCTCACTGGAATATATTAATTAATCTCTCTAGTCCCGTCTCTCTCATCATCT 1140
Db 1081 ACCAGAGCTCACTGGAATATATTAATTAATCTCTCTAGTCCCGTCTCTCTCATCATCT 1140

QY 1141 CTCACACAAACAAAAG 1158
Db 1141 CTCACACAAACAAAAG 1158
RESULT 2
US-09-998-059-13
Sequence 13, Application US/09998059
Publication No. US20030005485A1
GENERAL INFORMATION:
APPLICANT: Ohlrogge, John B.
APPLICANT: Benning, Christoph
APPLICANT: Gao, Hongdo
APPLICANT: Girke, Thomas
APPLICANT: White, Joseph A.
TITLE OF INVENTION: Plant Seed Specific Promoters
FILE REFERENCE: MSU-06689
CURRENT FILING DATE: US/09/998,059
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,401
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 1164
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-998-059-13
Query Match 100.0%; Score 1158; DB 10; Length 1164;
Best Local Similarity 100.0%; Pred. No. 4e-255;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACAAACATACCTGAAAAATCCAGACTCAGATCTACTGATTAATGCAACTTCATCATGAA 60
Db 1 CACAAACATACCTGAAAAATCCAGACTCAGATCTACTGATTAATGCAACTTCATCATGAA 60
QY 61 AACATCAAAAAAGTCAAAAGTAACAAAAATCAAGTGAATTCAGACACAAAGCCAGTAA 120
Db 61 AACATCAAAAAAGTCAAAAGTAACAAAAATCAAGTGAATTCAGACACAAAGCCAGTAA 120
QY 121 GATGAAAAATTTAAGAAAGCTGATGCTAAGCTGGCGAAAAATCTTCTTAATCAAAACAG 180
Db 121 GATGAAAAATTTAAGAAAGCTGATGCTAAGCTGGCGAAAAATCTTCTTAATCAAAACAG 180
QY 181 TAACACGAGTAATAGCAAAAAATCCGAGCAGAAAAATCTCAACCCAGCTCCGAAATTCACG 240
Db 181 TAACACGAGTAATAGCAAAAAATCCGAGCAGAAAAATCTCAACCCAGCTCCGAAATTCACG 240
QY 241 TCTTCACTAAATTTTCGAAAGAAATCGATCAATAACAAACCATTTACACAAATACATTA 300
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Db 301 TCAAAATGCGGAGAAATCTGTAAGCTGAAACCTTGTCAAGTCGACAGAGAGAGAAAAAG 360
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Db 361 AGATCGTGAAGAAAGGGGTTTAAAGCTGAGACTTCTATTTGAGTAATGGAG 420
QY 421 GTGTCACTTTTCGTTTGGAAATGAACTTGGGCTCAGCTTATGGGCTATTAGATAT 480
Db 421 GTGTCACTTTTCGTTTGGAAATGAACTTGGGCTCAGCTTATGGGCTATTAGATAT 480
QY 481 TGATGGGCTTTCTAGTAATACAAATTAAGTTATGGGCTTAAATTAATGAGCCATGT 540
Db 481 TGATGGGCTTTCTAGTAATACAAATTAAGTTATGGGCTTAAATTAATGAGCCATGT 540
QY 541 TGAATAATTTTGAACATGCTTTGGCTACTAGTCTAAACATGACAGCAAGCAAGTTGTCG 600
Db 541 TGAATAATTTTGAACATGCTTTGGCTACTAGTCTAAACATGACAGCAAGCAAGTTGTCG 600

QY 601 AGACAAGTCGACATATATCAATGATCAAAACAGCTAGTGTGCGCGCTCGCTCAT 660
DB 601 AGACAAGTCGACATATATCAATGATCAAAACAGCTAGTGTGCGCGCTCGCTCAT 660
QY 661 GTGTCACTTTTCTCTGTTTTTTTAAATTTTCAATAGTTCTTTTGTATTTCA 720
DB 661 GTGTCACTTTTCTCTGTTTTTTTAAATTTTCAATAGTTCTTTTGTATTTCA 720
QY 721 ATACAAATTTTGGCTGTATCTTGCAACCTCTGCATATGCGCAATATACGTAAAC 780
DB 721 ATACAAATTTTGGCTGTATCTTGCAACCTCTGCATATGCGCAATATACGTAAAC 780
QY 781 CTGTGATCTAATTTGTGTATTTGTTAAATTTAGATTCTATTTCTCGGTTTAAAG 840
DB 781 CTGTGATCTAATTTGTGTATTTGTTAAATTTAGATTCTATTTCTCGGTTTAAAG 840
QY 841 TGAATTAATATGATCATGTGTTAAACATTTGTAAAGTATGATTAATTAATTAATTT 900
DB 841 TGAATTAATATGATCATGTGTTAAACATTTGTAAAGTATGATTAATTAATTAATTT 900
QY 901 AGTGAATGATATCGTGAAGCAAAAATGATGATGATGATTTGATTTTGTCTATTTTG 960
DB 901 AGTGAATGATATCGTGAAGCAAAAATGATGATGATGATTTGATTTTGTCTATTTTG 960
QY 961 ACATATGCGAGAGTGTAGCTACGCGCATGAAATCAAGAGACACTTGTCTGACCTCACAG 1020
DB 961 ACATATGCGAGAGTGTAGCTACGCGCATGAAATCAAGAGACACTTGTCTGACCTCACAG 1020
QY 1021 AGTGAATGATATCGTGAAGCAAAAATGATGATGATGATTTGATTTTGTCTATTTTG 1080
DB 1021 AGTGAATGATATCGTGAAGCAAAAATGATGATGATGATTTGATTTTGTCTATTTTG 1080
QY 1081 ACCAGAGCTCATTTGACAAATATATTAATCTCTCCCAAGTCCGCTCTCTCATCTCATCT 1140
DB 1081 ACCAGAGCTCATTTGACAAATATATTAATCTCTCCCAAGTCCGCTCTCTCATCTCATCT 1140
QY 1141 CTCACACAACAAACAAAAG 1158
DB 1141 CTCACACAACAAACAAAAG 1158

RESULT 3
US-09-938-842A-4937

Sequence 4937, Application US/09938842A
Patent No. US20020160378B1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300, 111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4937
LENGTH: 1223
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-4937

Query Match 100.0%; Score 1158; DB 9; Length 1223;
Best Local Similarity 100.0%; Pred. No. 4, 1e-255;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAAACATACACTCAAAATCCAGACTCATCTACTCAATTAATGCACTTCATCAATGA 60
DB 63 CACAAACATACACTCAAAATCCAGACTCATCTACTCAATTAATGCACTTCATCAATGA 122
QY 61 AACATCAAAAACAGTCAAAAGTAAACAAATGCAAGTCAAGTTCAGCAGACAAAGCAGTAA 120
DB 123 AACATCAAAAACAGTCAAAAGTAAACAAATGCAAGTCAAGTTCAGCAGACAAAGCAGTAA 182
QY 121 GATGAAAATTTTACGAAAGCTCATGCTAAGCTGGCCAAAATATCTTCTTAATCAAAACAG 180
DB 183 GATGAAAATTTTACGAAAGCTCATGCTAAGCTGGCCAAAATATCTTCTTAATCAAAACAG 242
QY 181 TAACAAAGATTAATGCAAAATCCGAGCAAAAATCTCACCCACTTCGAAATTCACAG 240
DB 243 TAACAAAGATTAATGCAAAATCCGAGCAAAAATCTCACCCACTTCGAAATTCACAG 302
QY 241 TCTTCACTAAAATTTTGCAGAGAAATCGATCAATACCAACCAATTAACAAAATACATA 300
DB 303 TCTTCACTAAAATTTTGCAGAGAAATCGATCAATACCAACCAATTAACAAAATACATA 362
QY 301 TCAAAATGCGAGAAATCGTACCTGGAAACTTGTCAAGTGGCAGAGAGAGAAAAGGA 360
DB 363 TCAAAATGCGAGAAATCGTACCTGGAAACTTGTCAAGTGGCAGAGAGAGAAAAGGA 422
QY 361 AGATCGTGAGAGAAAGGGTTTAGGGTTTAAAGCTCAGACTTCTATTGAGTAAATGGAGC 420
DB 423 AGATCGTGAGAGAAAGGGTTTAGGGTTTAAAGCTCAGACTTCTATTGAGTAAATGGAGC 482
QY 421 GTGTCACTTTTCCGTTTGGAAATGAACTTTGGGCTCAGCTTAATGGCTATTAGATTT 480
DB 483 GTGTCACTTTTCCGTTTGGAAATGAACTTTGGGCTCAGCTTAATGGCTATTAGATTT 542
QY 481 TGAATGGCTTTTGAATTAATCAATATATTAATGATTTGGGCTTAATTAAGCCATGT 540
DB 543 TGAATGGCTTTTGAATTAATCAATATATTAATGATTTGGGCTTAATTAAGCCATGT 602
QY 541 TGAATTAATTTGACACATGCTCTTGGCTACTAGTGTAAACATGCAACCGAAGCTTGTG 600
DB 603 TGAATTAATTTGACACATGCTCTTGGCTACTAGTGTAAACATGCAACCGAAGCTTGTG 662
QY 601 AGACAAGTCGACATATATCAATGATCAAAACAGCTTAGTGTGCGCGCTCTCGCTCAT 660
DB 663 AGACAAGTCGACATATATCAATGATCAAAACAGCTTAGTGTGCGCGCTCTCGCTCAT 722
QY 661 GTGTCACTTTTCTCTGTTTTTTTAAATTTTCAATAGTTCTTTTGTATTTCA 720
DB 723 GTGTCACTTTTCTCTGTTTTTTTAAATTTTCAATAGTTCTTTTGTATTTCA 782
QY 721 ATACAAATTTTGGCTGTATCTTGCAAACTCTTCATCATATGCGCAATATACGTAAAC 780
DB 783 ATACAAATTTTGGCTGTATCTTGCAAACTCTTCATCATATGCGCAATATACGTAAAC 842
QY 781 CTGTGATCTAATTTGTGTATTTGTTAAATTTAGATTCTATTTCTCGGTTTAAAG 840
DB 843 CTGTGATCTAATTTGTGTATTTGTTAAATTTAGATTCTATTTCTCGGTTTAAAG 902
QY 841 TGAATTAATATGATGATGTTAAACATTTGATGATGATGATTAATTAATTAATTT 900
DB 903 TGAATTAATATGATGATGTTAAACATTTGATGATGATGATTAATTAATTAATTT 962
QY 901 AGTGAATGATATCGTGAAGCAAAAATGATGATGATGATTTGATTTGTGTATTTTG 960
DB 963 AGTGAATGATATCGTGAAGCAAAAATGATGATGATGATTTGATTTGTGTATTTTG 1022
QY 961 ACATATGCGAGAGTGTAGCTACGCGCATGAAATCAAGAGACACTTGTCTGAGCTCACAG 1020
DB 1023 ACATATGCGAGAGTGTAGCTACGCGCATGAAATCAAGAGACACTTGTCTGAGCTCACAG 1082
QY 1021 AGTGAATGATTAAGGCTTAGCTGAAGTCCCATGCAAACTTAATCCATGAGTGTCAA 1080
DB 1083 AGTGAATGATTAAGGCTTAGCTGAAGTCCCATGCAAACTTAATCCATGAGTGTCAA 1142
QY 1081 ACCAGAGCTCATTTGACAAATATATTAATCTCTCTTAAGTCCGCTCTTCTCATCATCT 1140

Db 1143 ACCAGAGCTCAGTGAATATATACTCCTCAAGTCCCGTCTTCATCATCT 1202
Qy 1141 CTCACACAAACAAAAG 1158
Db 1203 CTCACACAAACAAAAG 1220

RESULT 4

US-09-938-842A-4937
; Sequence 4937, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4937
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4937

Query Match 100.0%; Score 1158; DB 11; Length 1223;
Best Local Similarity 100.0%; Pred. No. 4,1e-255;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CACAAACATACATCAAAATCCAGACTCATCTCAATATGCAATTCATCATGAA 60
Db 63 CACAAACATACATCAAAATCCAGACTCATCTCAATATGCAATTCATCATGAA 122
Qy 61 AACATCAAAAACAGTCAAAAGTAACAAAATCAAGTCAAGTTCAGACACAAACGAGTAA 120
Db 123 AACATCAAAAACAGTCAAAAGTAACAAAATCAAGTCAAGTTCAGACACAAACGAGTAA 182
Qy 121 GATAGAAAATTTAAGAAAGCTCATGCTAAGCTGGCGAAAATTAATCTTCTAATCAAAACAG 180
Db 183 GATAGAAAATTTAAGAAAGCTCATGCTAAGCTGGCGAAAATTAATCTTCTAATCAAAACAG 242
Qy 181 TAACAAGAGTAATAGCAAAATCCGAGAGAAAATCTCAACCCACTCCGAAATTCACG 240
Db 243 TAACAAGAGTAATAGCAAAATCCGAGAGAAAATCTCAACCCACTCCGAAATTCACG 302
Qy 241 TCTTCACTAAATTTTCGAAAGAAATCGATCAATAACAAACCATTAACAACAAATACATTA 300
Db 303 TCTTCACTAAATTTTCGAAAGAAATCGATCAATAACAAACCATTAACAACAAATACATTA 362
Qy 301 TCAAAATGCGGAGATTCGTAAGTCTGAAACTTCTTCAAGTGGCAGAGAGAGAAAAGGA 360
Db 363 TCAAAATGCGGAGATTCGTAAGTCTGAAACTTCTTCAAGTGGCAGAGAGAGAAAAGGA 422
Qy 361 AGATGCGAGAAAGGGGTTTAGGGTTAAGCTCAGACTTCATTGAGTAAGGAGAG 420
Db 423 AGATGCGAGAAAGGGGTTTAGGGTTAAGCTCAGACTTCATTGAGTAAGGAGAG 482
Qy 421 GTGTCAATTTTCGTTTGGAAATGAATCTTGGGCTCAGCTTATGGGCTATTAGATAT 480
Db 483 GTGTCAATTTTCGTTTGGAAATGAATCTTGGGCTCAGCTTATGGGCTATTAGATAT 542
Qy 481 TGATGGGCTTTAGTAATATACATATTAAGTTATGGGCTTATGTTAAATAAGCCATGT 540

Db 543 TGATGGGCTTTAGTAATATACATATTAAGTTATGGGCTTATGTTAAATAAGCCATGT 602
Qy 541 TGAATAATTTTGAACATGCTCTTGAGCTACTAGTCTAAACATGCAACGAGATGTCG 600
Db 603 TGAATAATTTTGAACATGCTCTTGAGCTACTAGTCTAAACATGCAACGAGATGTCG 662
Qy 601 AGACAAGTCGAGCATATACATATGATCAACACGCTTAGTGGCGGCTCTGCTCAT 660
Db 663 AGACAAGTCGAGCATATACATATGATCAACACGCTTAGTGGCGGCTCTGCTCAT 722
Qy 661 GTGTCACTTTTCCGCTTTTCTTTTAAATTTTCAAAATCTCTTTTGTATTTTCA 720
Db 723 GTGTCACTTTTCCGCTTTTCTTTTAAATTTTCAAAATCTCTTTTGTATTTTCA 782
Qy 721 ATACAAATTTTGGCTGATCTTCAAACTCTTGATCATATCCCAATATACGTAACA 780
Db 783 ATACAAATTTTGGCTGATCTTCAAACTCTTGATCATATCCCAATATACGTAACA 842
Qy 781 CTGTGATCTAATTTGTTGTTAATTGTTAATTTAGATTCTATTCGCGTTTAAAG 840
Db 843 CTGTGATCTAATTTGTTGTTAATTGTTAATTTAGATTCTATTCGCGTTTAAAG 902
Qy 841 TGAATTAATGATATCATGCTTAAACATGTAAGTAAGTAAGTAATTAATTAATTT 900
Db 903 TGAATTAATGATATCATGCTTAAACATGTAAGTAAGTAATTAATTAATTAATTT 962
Qy 901 AGTTGATGATTAAGTGAAGCAAAAATGAGATAGATCATTTGATTTTGTCTATTTTG 960
Db 963 AGTTGATGATTAAGTGAAGCAAAAATGAGATAGATCATTTGATTTTGTCTATTTTG 1022
Qy 961 ACATATGCGAGAGTGAAGCTACGCGCATGAAGATCAAGACACTGCTGAGCTCACAG 1020
Db 1023 ACATATGCGAGAGTGAAGCTACGCGCATGAAGATCAAGACACTGCTGAGCTCACAG 1082
Qy 1021 AGTACGCTTAAAGCTTAAGCTGAAGTCCCGCATGCAAACTAATCTAGTGGCTCAA 1080
Db 1083 AGTACGCTTAAAGCTTAAGCTGAAGTCCCGCATGCAAACTAATCTAGTGGCTCAA 1142
Qy 1081 ACCAGAGCTCACTGACATATATTAATCTCTTAAGTCCGTTCTCTTCATCATCT 1140
Db 1143 ACCAGAGCTCACTGACATATATTAATCTCTTAAGTCCGTTCTCTTCATCATCT 1202
Qy 1141 CTCACACAAACAAAAG 1158
Db 1203 CTCACACAAACAAAAG 1220

RESULT 5

US-10-892-513-4
; Sequence 4, Application US/10892513
; Publication No. US20050039229A1
; GENERAL INFORMATION:
; APPLICANT: Unilever Ltd
; TITLE OF INVENTION: Double recoverable block of function
; FILE REFERENCE: Kuvshinov double construct
; CURRENT APPLICATION NUMBER: US/10/892,513
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 09/617,543
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1183
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Brassica napus
; NAME/KEY: misc feature
; OTHER INFORMATION: CRU promoter with artificial polyadenylation site
US-10-892-513-4

Query Match 17.2%; Score 198.8; DB 21; Length 1183;

Best Local Similarity 66.0%; Pred. No. 3,4e-35;
Matches 409; Conservative 0; Mismatches 177; Indels 34; Gaps 7;
QY 568 ACTAGTCTTAACATGCAACGAGTTGTCGACCAAGTCAGATATACATGAT 627
DB 567 ACTGCTCTTGAATGCAACGAGTTGTCGACCAAGTCAGATATACATGAT 626
QY 628 CAACACGCTAGTGTGCGCGCTCTGCTCATGTGTCACTTGTCTCTGTTTTTT 687
DB 627 CAACACCTCGAGTGTGCGCGCTCTGCTCATGTGTCACTTGTCTCTCTT--TCC 682
QY 688 TAATTTTCAATAGTTCTTTTGTATATCTTCAATACAAATTTTGGCTGTATCTGCA 747
DB 683 TAAATAATGTATCTAATTTTCAAAAAAGAGAGATGTTTGGCTGTATCTCTTAA 742
QY 748 ACTCTGATCATATGCGCA-----ATATACGGAACACTGGGATCTAATTTGTTG 801
DB 743 ACTATTCGATCAACAGCGCATATTTTAACTGATCTAGTATGATGATTTG 802
QY 802 TTAATTTGT-TAAATTTAGATTTCTCGGTTTAAAGTGAATTAATGATGATGAT 860
DB 803 TTAATTTGTCAAAAAGTATGATTTCTCTATCTGTTTTTAAATTAATGATGATGAT 862
QY 861 TAAACATTTGTAAGTATGATTAATTAATTAATTTTAAATTTGATGATTAACGTAAG 920
DB 863 TGAATTTAAATGATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 922
QY 921 -----CAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
DB 923 CTGATTAACATGAACCATTTTCTTAAAAATGATGATGATGATGATGATGATGATGAT 982
QY 960 GACATATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
DB 983 GAGTATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1042
QY 1020 GAGTATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1079
DB 1043 GAGTATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1102
QY 1080 AACCAAGAGCTCTGACATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1137
DB 1103 AACCTTCAATGCTACCTCCATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1162
QY 1138 TCTCTCAACAACAACAAAA 1157
DB 1163 TCTATCAAAAAACACACAA 1182
RESULT 6
US-10-892-513-10
; Sequence 10, Application US/10892513
; Publication No. US20050039229A1
; GENERAL INFORMATION:
; APPLICANT: Unicep Ltd
; TITLE OF INVENTION: Double recoverable block of function
; FILE REFERENCE: Kuvshinov double construct
; CURRENT APPLICATION NUMBER: US/10/892,513
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 09/617,543
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent version 3.2
; SEQ ID NO 10
; LENGTH: 1293
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Braesica napus
; NAME/KEY: misc feature
; LOCATION: (1)-(1239)
; OTHER INFORMATION: Changed CRU promoter with three tet operators in the vicinity of
; APPLICANT: TATA box

FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1226)-(1244)
; OTHER INFORMATION: Tet operator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1246)-(1252)
; OTHER INFORMATION: Tata-box
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1254)-(1272)
; OTHER INFORMATION: Tet operator
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1275)-(1293)
; OTHER INFORMATION: Tet operator
US-10-892-513-10
Query Match 17.2%; Score 198.8; DB 21; Length 1293;
Best Local Similarity 66.0%; Pred. No. 3,6e-35;
Matches 409; Conservative 0; Mismatches 177; Indels 34; Gaps 7;
QY 568 ACTAGTCTTAACATGCAACGAGTTGTCGACCAAGTCAGATATACATGAT 627
DB 567 ACTGCTCTTGAATGCAACGAGTTGTCGACCAAGTCAGATATACATGAT 626
QY 628 CAACACGCTAGTGTGCGCGCTCTGCTCATGTGTCACTTGTCTCTGTTTTTT 687
DB 627 CAACACCTCGAGTGTGCGCGCTCTGCTCATGTGTCACTTGTCTCTCTT--TCC 682
QY 688 TAATTTTCAATAGTTCTTTTGTATATCTTCAATACAAATTTTGGCTGTATCTGCA 747
DB 683 TAAATAATGTATCTAATTTTCAAAAAAGAGATGATGATGATGATGATGATGATGAT 742
QY 748 ACTCTGATCATATGCGCA-----ATATACGGAACACTGGGATCTAATTTGTTG 801
DB 743 ACTATTCGATCAACAGCGCATATTTTAACTGATCTAGTATGATGATTTG 802
QY 802 TTAATTTGT-TAAATTTAGATTTCTCGGTTTAAAGTGAATTAATGATGATGATGAT 860
DB 803 TTAATTTGTCAAAAAGTATGATTTCTCTATCTGTTTTTAAATTAATTAATTAATTAAT 862
QY 861 TAAACATTTGTAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 920
DB 863 TGAATTTAAATGATTAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 922
QY 921 -----CAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
DB 923 CTGATTAACATGAACCATTTTCTTAAAAATGATGATGATGATGATGATGATGATGAT 982
QY 960 GACATATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
DB 983 GAGTATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1042
QY 1020 GAGTATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1079
DB 1043 GAGTATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1102
QY 1080 AACCAAGAGCTCTGACATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1137
DB 1103 AACCTTCAATGCTACCTCCATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1162
QY 1138 TCTCTCAACAACAACAAAA 1157
DB 1163 TCTATCAAAAAACACACAA 1182
RESULT 7
US-10-311-455-2139/c
; Sequence 2139, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander

APPLICANT: PIERENROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2139
LENGTH: 10326
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2139

Query Match
Best Local Similarity 5.6%; Score 65.4; DB 15; Length 10326;
Matches 177; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 2 ACAAACATACCTCAAAATCCAGACTCACTCTCAATTATGCAACTTCATCATGAA 61
DB 2764 ACCAATCTAATCCAAAACCACTAAATTAATTAACCTAAACAAAATTTCAACAT 2705
QY 62 ACATCAAAAACGTCAAAATGAAATCAATGATGATTCAGACACAAAGCCAGTAAAG 121
DB 2704 TCACCTCAAAACAAAAATTTCTACTTAATAATCAAAACAAACAAACAAATTA 2645
QY 122 ATAGAAATTTAAGCAGCTCATGCTAGCTGCGCAAAATCTCTCAATGAAACAGT 181
DB 2644 AAAAAATTTTAAACACCTCCAAAATAATTAACAAACACAAATCTCAACATATA 2585
QY 182 AACAAAGATTAATGACAAATCCAGACGAAACCTCCACCCCTCGAAATTCAGT 241
DB 2584 TACCAATTCATCTTAATTAATAAAGCAATTTTCAACAGCATTAATAAATAATACGA 2525
QY 242 CTTCCTAAATTTTGGAAAGGATGATCAATACCAACCCCTTACCAAAATACATAT 301
DB 2524 TATCACCCTACTTAAAAAATAATCAATCAATAAATAATTAATTAATTAAT 2465
QY 302 CAAATGGCGAATCGTACTCGAAACTTCTCAAGTCGACAGAGAGAGAAAGGA 361
DB 2464 TAAATAATTAACAAAAATTTTAAACAAATATCTCTACTACTCAATATATAAATAA 2405
QY 362 GAT 364
DB 2404 TAT 2402

RESULT 8
US-10-021-323-16890/c

Sequence 16890, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 16890

LENGTH: 547
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3829-025-Q6-N6-C2
US-10-021-323-16890

Query Match
Best Local Similarity 5.5%; Score 64.2; DB 19; Length 547;
Matches 138; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 680 TTTTCTTAAATTTTCAATAGTCTTTGTTTATCTCAATCAATTTTGGCTGTA 739
DB 350 TTTTCTTAAATTTTCAATAGTCTTTGTTTATCTCAATCAATTTTGGCTGTA 291
QY 740 TCTTCAAACTCTGATCATATCGCAATATAGTGACACATGATCAATTTGTTG 799
DB 290 TTTTCAAAATTTTCCCTTTTCCCTTTTCTTTTAAATTTTCTTTTCTTTT 231
QY 800 TGTAAATGTTAAATTAATGATCTATCTCGGTTTAAAGTGAATTAATGATCATG 859
DB 230 TTTTCTTAAATTTTCAATAGTCTTTGTTTATCTCAATCAATTTTGGCTGTA 171
QY 860 TTAATAACATGTTAGTATGATGATTAATAATGATTAATTTAGTTGATGATTAACGTA 919
DB 170 AAAAAAATTTTCAATAGTCTTTGTTTATCTCAATCAATTTTGGCTGTA 111
QY 920 GCAAAAAATGATGATGATCA 940
DB 110 AAAAAAATTTTCAATAGTCTTTGTTTATCTCAATCAATTTTGGCTGTA 90

RESULT 9
US-10-021-323-6681/c

Sequence 6681, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 6681
LENGTH: 433
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3828-009-Q1-N6-D11
US-10-021-323-6681

Query Match
Best Local Similarity 4.9%; Score 56.4; DB 19; Length 433;
Matches 141; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 657 TCATGTGACCTGTTTCTCGTTTCTTTTAAATTTTCAATGATCTTTGTTATC 716
DB 282 TTAATGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 223
QY 717 TTCAATACAAATTTTGGCTGATCTGCAACCTTCGATCATATGCCAATATAGTG 776
DB 222 TTTTCAATACAAATTTTGGCTGATCTGCAACCTTCGATCATATGCCAATATAGTG 163
QY 777 AACACTGGATCTAATTTGTTGTTAATGTTAATTTAGATTTCTCCGCTTGA 836
DB 162 TTTTCTTAAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 103

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